

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: December 12, 2005, 00:31:12 ; Search time 119.491 Seconds
(without alignments)
96.991 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31
Sequence: 1 tccgcaccggaagttgagtagacggtgctg 31

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

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*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	11029	6 US-10-714-781A-66	Sequence 66, Appl
2	20.4	65.8	164527	7 US-11-121-086-71	Sequence 71, Appl
3	18.4	59.4	750	7 US-11-056-825-3	Sequence 3, Appl
4	18.4	59.4	750	7 US-11-056-825-6	Sequence 6, Appl
5	17.4	56.1	1130	7 US-11-000-463-488	Sequence 488, App
6	17.4	56.1	1130	7 US-10-750-185-33268	Sequence 33268, A
7	17.4	56.1	1600	7 US-11-000-463-16	Sequence 16, Appl
8	17.4	56.1	2891	6 US-10-821-234-84	Sequence 84, Appl
9	17.2	55.5	1395	7 US-11-055-822-1035	Sequence 1035, Ap
10	17.2	55.5	1082144	7 US-11-117-187-211	Sequence 211, App
11	17	54.8	777	6 US-10-512-184-9	Sequence 9, Appl
12	17	54.8	1113	6 US-10-512-184-60	Sequence 60, Appl
13	17	54.8	1881	6 US-10-512-184-24	Sequence 24, Appl
14	16.8	54.2	2313	7 US-11-000-165-51	Sequence 51, Appl
15	16.8	54.2	2313	7 US-11-032-794-51	Sequence 51, Appl
16	16.8	54.2	175673	7 US-11-121-086-55	Sequence 55, Appl
17	16.6	53.5	862	6 US-10-750-185-37736	Sequence 37736, A
18	16.6	53.5	1413	7 US-11-055-822-959	Sequence 959, App
19	16.6	53.5	1413	6 US-10-750-185-34369	Sequence 34369, A
20	16.6	53.5	1726	6 US-10-750-185-35332	Sequence 35332, A
21	16.6	53.5	1804	6 US-10-750-185-31994	Sequence 31994, A
22	16.6	53.5	149419	7 US-11-112-908-49	Sequence 49, Appl
23	16.6	53.5	157224	7 US-11-112-908-51	Sequence 51, Appl

24	16.6	53.5	161726	7 US-11-112-908-48	Sequence 48, Appl
25	16.6	53.5	161726	7 US-11-112-908-52	Sequence 52, Appl
26	16.6	53.5	178877	7 US-11-121-086-17	Sequence 17, Appl
27	16.4	52.9	156297	7 US-11-121-086-65	Sequence 65, Appl
28	16.4	52.9	171423	7 US-11-121-086-85	Sequence 85, Appl
29	16.4	52.9	175416	7 US-11-121-086-43	Sequence 43, Appl
30	16.2	52.3	600	6 US-10-750-185-507	Sequence 507, App
31	16.2	52.3	600	6 US-10-750-185-1980	Sequence 1980, Ap
32	16.2	52.3	699	6 US-10-750-185-47086	Sequence 47086, A
33	16.2	52.3	981	6 US-10-858-730-136	Sequence 136, App
34	16.2	52.3	2356	6 US-10-750-185-46730	Sequence 46730, A
35	16.2	52.3	3138	6 US-10-392-234A-15	Sequence 15, Appl
36	16.2	52.3	3187	6 US-10-821-234-69	Sequence 69, Appl
37	16.2	52.3	3336	6 US-10-750-185-45825	Sequence 45825, A
38	16.2	52.3	162289	7 US-11-121-086-20	Sequence 20, Appl
39	16	51.6	438	7 US-11-012-353-51	Sequence 51, Appl
40	16	51.6	3754	6 US-10-750-185-48934	Sequence 48934, A
41	16	51.6	184000	7 US-11-121-086-37	Sequence 37, Appl
42	15.8	51.0	855	6 US-10-750-185-56888	Sequence 56888, A
43	15.8	51.0	1632	6 US-10-750-185-38126	Sequence 38126, A
44	15.8	51.0	1741	7 US-11-000-463-97	Sequence 97, Appl
45	15.8	51.0	2134	6 US-10-750-185-57401	Sequence 57401, A

ALIGNMENTS

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RESULT 1
US-10-714-781A-66
; Sequence 66, Application US/10714781A
; Publication No. US20050255127A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINKE, JULES MARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714, 781A
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679, 520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374, 953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116, 298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281, 923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676, 502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-714-781A-66

Query Match          96.8%; Score 30; DB 6; Length 11029;
Best Local Similarity 100.0%; Pred.No. 0.00019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 CCGCCACCGAAGTGTGATGACGCGTCTG 31
DB      10523 CCGCCACCGAAGTGTGATGACGCGTCTG 10552
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RESULT 2
US-11-121-086-71
; Sequence 71, Application US/11121086
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; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 0918.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 164527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-71

Query Match      65.8%; Score 20.4; DB 7; Length 164527;
Best Local Similarity 80.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 CCGCACCGGAAGTTGATGACGGTCTG 31
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Db      66059 CCTCACCGGAAGTTGAGAGATGCTG 66088

RESULT 3
US-11-056-825-3/c
; Sequence 3, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Feilding-Habermann, Brunnhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SCR-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; SOFTWARE: PatentIn version 3.3
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: CDS
; LOCATION: (1)..(750)
US-11-056-825-3

Query Match      59.4%; Score 18.4; DB 7; Length 750;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAGTTGATGACGGTG 28
        |||||||
Db      375 TCCGCCACCGCGCCCTGAGAGACGGTG 348

RESULT 4
US-11-056-825-6/c
; Sequence 6, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Feilding-Habermann, Brunnhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SCR-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-6

Query Match      59.4%; Score 18.4; DB 7; Length 750;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 TCCGCCACCGGAAGTTGATGACGGTG 28
        |||||||
Db      375 TCCGCCACCGCGCCCTGAGAGACGGTG 348

RESULT 5
US-11-000-463-488
; Sequence 488, Application US/11000463
; Publication No. US2005026423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radjoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 488
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-488

Query Match      56.1%; Score 17.4; DB 7; Length 1130;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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PRIORITY FILING DATE: 1999-07-02
PRIORITY APPLICATION NUMBER: 60/148,613
PRIORITY FILING DATE: 1999-08-12
PRIORITY APPLICATION NUMBER: 60/187,970
PRIORITY FILING DATE: 2000-03-09
PRIORITY APPLICATION NUMBER: DE 19930476.9
PRIORITY FILING DATE: 1999-07-01
PRIORITY APPLICATION NUMBER: DE 19931415.2
PRIORITY FILING DATE: 1999-07-08
PRIORITY APPLICATION NUMBER: DE 19933148.7
PRIORITY FILING DATE: 1999-07-08
PRIORITY APPLICATION NUMBER: DE 199331419.5
PRIORITY FILING DATE: 1999-07-08
PRIORITY APPLICATION NUMBER: DE 199331420.9
PRIORITY FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 1035
LENGTH: 1395
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1372)
OTHER INFORMATION: RXA01483
US-11-055-822-1035

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Query Match	55.5%	Score 17.2 ;	DB 7 ;	Length 1395 ;
Best Local Similarity	73.3%	Pred. No. 60 ;		
Matches 22 ;	Conservative 0 ;	Mismatches 8 ;	Indels 0 ;	Gaps 0

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QY      2  CCGCCACCCGGAAGTTGAGTAGACGGTGCTG  31
          ||| ||| ||| ||| ||| ||| ||| |||
DB      917 CCACCACCGGAAGTCCCGCAACGATGCTG  888

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```

RESULT 10
US-11-117-187-211/C
Sequence 211, Application US/11117187
Publication No. US2005026560A1
GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD-309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 211
LENGTH: 1082144
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-11-117-187-211

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Query Match	55.5%	Score 17.2	DB 7	Length 1082144
Best Local Similarity	86.4%	Pred. No. 1.4e+02		
Matches 19	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY		1	TCCGCCACCGGAAGTTGACTAG	22
Db		364367	TCCCACATCGGAAGTTGACTAG	364346

RESULT 11
US-10-512-184-9/c
; Sequence 9, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:

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? APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
? TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
? TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
? TITLE OF INVENTION: resistance against fungi
? FILE REFERENCE: 3581_01US01
? CURRENT APPLICATION NUMBER: US/10/512.184
? CURRENT FILING DATE: 2004-10-22
? NUMBER OF SEQ ID NOS: 72
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 9
? LENGTH: 777
? TYPE: DNA
? ORGANISM: Artificial Sequence
FEATURES:
? OTHER INFORMATION: Description of Artificial Sequence: seqv pl2 with
? OTHER INFORMATION: specificity against Phoma lingam; originates from
? US-10-512-184-9

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Query Match	54.8%	Score 17;	DB 6;	Length 777;
Best Local Similarity	80.0%	Pred. No. 91;		
Matches 20;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0

QY 7 ACCGGAAGTTGAGTAGACCGGCTGCTG 31
Db 593 ACCAGAAGTTAGGAGACTGTCCTG 565

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RESULT 12
US-10-512-184-60/c
; Sequence 60, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fizinhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising ACE - linker - scFv PL2.
US-10-512-184-60

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Query Match	54.8%	Score 17	DB 6	Length 1113
Best Local Similarity	80.0%	Pred. No. 95		
Matches 20	Conservative 0	Mismatches 5	Indels 0	Gaps 0

QY 7 ACCGGAAGTTGAGTAGACCGGTGCTG 31
Db 929 ACCAGAAGTTAGGAGACTGTCCCTG 905

RESULT 13
 US-10-512-184-24/C
 ; Sequence 24, Application US/10512184
 ; Publication No. US20050244901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
 ; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
 ; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
 ; FILE REFERENCE: 3581.01US01
 ; CURRENT APPLICATION NUMBER: US/10/512,184
 ; CURRENT FILING DATE: 2004-10-22
 ; NUMBER OF SEQ ID NOS: 72

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising leader peptide - chitinase - linker -
; OTHER INFORMATION: scfv PL2 - cmvC/HIS6.
US-10-512-184-24

Query Match          54.2%; Score 16.8; DB 7; Length 2313;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 ACCGGAAGTGTAGTACGGTGCTG 31
DB 1616 ACCGGAAGTGTAGGAGCTGTCTG 1592

RESULT 14
US-11-000-365-51/c
; Sequence 51, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; FILE REFERENCE: 21459-97705
; CURRENT APPLICATION NUMBER: US/11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 51
; LENGTH: 2313
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-000-365-51

Query Match          54.2%; Score 16.8; DB 7; Length 2313;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCACCGAAGTGTAGTACGGTGCTG 31
DB 1266 GCTACCTGAAGAGGCGAGATGTGCTG 1239

RESULT 15
US-11-032-794-51/c
; Sequence 51, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
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; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97816
; CURRENT APPLICATION NUMBER: US/11/032,794
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 51
; LENGTH: 2313
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-032-794-51

Query Match          54.2%; Score 16.8; DB 7; Length 2313;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCACCGAAGTGTAGTACGGTGCTG 31
DB 1266 GCTACCTGAAGAGGCGAGATGTGCTG 1239
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Job time: 120.491 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 21:35:42 ; Search time 81.1636 Seconds
(Without alignments)
678.930 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31
Sequence: 1 tccgcaccggaagtgtgacgctgctg 31

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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9: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.8	63.9	1806	3	US-09-252-991A-15978
2	19.8	63.9	2289	3	US-09-252-991A-16301
3	19.6	63.2	111	3	US-08-454-098-5
4	19.6	63.2	111	6	PCT-US96-01600-5
C 5	19	61.3	436	3	US-09-464-535-13
C 6	19	61.3	480	3	US-09-318-786-36
C 7	19	61.3	600	3	US-09-464-535-39
C 8	19	61.3	673	3	US-09-464-535-31
C 9	19	61.3	1578	3	US-09-351-224E-7
C 10	19	61.3	1578	3	US-09-677-488A-7
C 11	19	61.3	1578	3	US-09-677-682B-7
C 12	19	61.3	1578	3	US-09-882-694B-7
C 13	19	61.3	1764	3	US-09-351-224E-6
C 14	19	61.3	1764	3	US-09-677-488A-6
C 15	19	61.3	1764	3	US-09-677-682B-6
C 16	19	61.3	1764	3	US-09-882-694B-6
C 17	18.8	60.6	1309	3	US-09-270-767-11451
C 18	18.8	60.6	1846	3	US-09-270-767-14186
C 19	18.8	60.6	22761	3	US-09-902-540-1219
C 20	18.6	60.0	601	3	US-09-949-016-23874
C 21	18.6	60.0	601	3	US-09-949-016-197817
C 22	18.6	60.0	601	3	US-09-949-016-197864
C 23	18.6	60.0	51927	3	US-09-949-016-17347
C 24	18.6	60.0	51927	3	US-09-949-016-17348

25	18.6	60.0	73853	3	US-09-949-016-12029	Sequence 12029, A
26	18.4	59.4	49	2	US-08-726-528A-7	Sequence 7, Appl1
C 27	18.4	59.4	601	3	US-09-949-016-52563	Sequence 52563, A
C 28	18.4	59.4	660	3	US-09-533-559-7236	Sequence 7236, Ap
C 29	18.4	59.4	668	3	US-09-533-559-6969	Sequence 6969, Ap
C 30	18.4	59.4	875	3	US-09-533-559-7730	Sequence 7730, Ap
C 31	18.2	58.7	720	2	US-08-459-354-3	Sequence 3, Appl1
C 32	18.2	58.7	720	2	US-08-077-253-3	Sequence 3, Appl1
C 33	18.2	58.7	720	3	US-08-333-840-3	Sequence 3, Appl1
C 34	18.2	58.7	975	3	US-10-668-047A-3	Sequence 3, Appl1
35	18.2	58.7	975	3	US-09-248-796A-5867	Sequence 5867, Ap
36	18	58.1	4494	3	US-09-902-540-659	Sequence 659, App
C 37	17.8	57.4	530	3	US-09-533-559-2601	Sequence 2601, Ap
C 38	17.8	57.4	601	3	US-09-949-016-70199	Sequence 70199, A
C 39	17.8	57.4	969	3	US-09-188-930-11	Sequence 11, Appl1
40	17.8	57.4	969	3	US-09-312-283C-11	Sequence 11, Appl1
41	17.8	57.4	2343	3	US-09-902-540-6663	Sequence 6663, Ap
42	17.8	57.4	2730	3	US-09-489-039A-6744	Sequence 6744, Ap
C 43	17.8	57.4	3247	3	US-09-902-540-526	Sequence 526, App
C 44	17.8	57.4	9225	3	US-09-543-681A-1336	Sequence 1336, Ap
45	17.8	57.4	50062	3	US-09-949-016-13809	Sequence 13809, A

ALIGNMENTS

RESULT 1
US-09-252-991A-15978/C
; Sequence 15978, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15978
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15978

Query Match 63.9%; Score 19.8; DB 3; Length 1806;
Best Local Similarity 77.4%; Pred. No. 21;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTGTGACGCTGCTG 31
Db 538 TTCGCCACCGGAAGTGTGACGCTG 508

RESULT 2
US-09-252-991A-16301
; Sequence 16301, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 16301
LENGTH: 2289
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16301

Query Match
Best Local Similarity 63.2%; Score 19.8; DB 3; Length 2289;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGAAGTGTAGACGGTCTG 31
Db 1992 TTCGCCACCGAAGCGAGTGGCGCAGCTG 2022

RESULT 3
US-08-454-098-5
Sequence 5, Application US/08454098
Patent No. 6103521
GENERAL INFORMATION:

APPLICANT: CAPON, DANIEL J
APPLICANT: SMITH, DOUGLAS H
APPLICANT: TIAN, HUAN
APPLICANT: WINSLOW, GENINE A
APPLICANT: SIEKEVITZ, MIRIAM
TITLE OF INVENTION: MULTISPECIFIC CHIMERIC RECEPTORS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: CELL GENESYS, INC.
STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: US

ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,098
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/384,033
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-9600 x131
TELEFAX: (415) 349-7392
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-098-5

Query Match
Best Local Similarity 63.2%; Score 19.6; DB 3; Length 111;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CCGCACCGAAGTGTAGACGGTCTG 28
Db 81 CGTCACCGGAAGATGAGAGACGGTGT 106

RESULT 4
PCT-US96-01600-5*

Sequence 5, Application PC/TUS9601600
GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.
APPLICANT: Smith, Douglas H.
APPLICANT: Tian, Huan
APPLICANT: Winslow, Genine A.
APPLICANT: Siekevitz, Miriam
TITLE OF INVENTION: Multispecific Chimeric Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01600
FILING DATE: 06-FEB-1996
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7639-051-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-01600-5

Query Match
Best Local Similarity 63.2%; Score 19.6; DB 6; Length 111;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CCGCACCGAAGTGTAGACGGTCTG 28
Db 81 CGTCACCGGAAGATGAGAGACGGTGT 106

RESULT 5
US-09-464-535-13/C
Sequence 13, Application US/09464535
Patent No. 6545200
GENERAL INFORMATION:

APPLICANT: Famodu, Omolayo O.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Sakai, Hajime
APPLICANT: McGonigle, Brian
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
FILE REFERENCE: BB1306 US NA
CURRENT APPLICATION NUMBER: US/09/464,535
CURRENT FILING DATE: 1999-12-15
EARLIER APPLICATION NUMBER: 60/112,555
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 436
TYPE: DNA
ORGANISM: Triticum aestivum

US-09-464-535-13

Query Match 61.3%; Score 19; DB 3; Length 436;
Best Local Similarity 81.5%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CCACCGGAAGTTGAGTAGACGGTGTG 31
Db 157 CCACCGGAAGTTGAGTAGACCGAGTGTG 131

RESULT 6
US-09-318-786-36/C

; Sequence 36, Application US/09318786
; Patent No. 6472147
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D
; APPLICANT: Wirsching, Peter
; APPLICANT: Lerner, Richard A
; APPLICANT: Gao, Changshou
; TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
; TITLE OF INVENTION: FILAMENTOUS PHASE USING PVIIT AND PIX, COMPOSITIONS,
; TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
; FILE REFERENCE: TSO3055
; CURRENT APPLICATION NUMBER: US/09/318,786
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: encoding fusion polypeptide
US-09-318-786-36

Query Match 61.3%; Score 19; DB 3; Length 490;
Best Local Similarity 81.5%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGTG 28
Db 371 CCACCGACCGAAGTTGAGTAGACGGTGTG 345

RESULT 7
US-09-464-535-39/C

; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McConigle, Brian
; APPLICANT: Rafaleki, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BBI306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Trilicium aestivum
US-09-464-535-39

Query Match 61.3%; Score 19; DB 3; Length 600;
Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 CCACCGGAAGTTGAGTAGACGGTGTG 31
Db 164 CCACCGGAAGTTGAGTAGACCGAGTGTG 138

RESULT 8
US-09-464-535-31/C

; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McConigle, Brian
; APPLICANT: Rafaleki, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BBI306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (95)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (385)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (388)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (487)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (554)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (557)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (560)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (626)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (634)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (650)

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FEATURE:
NAME/KEY: unsure
LOCATION: (664)
FEATURE:
NAME/KEY: unsure
LOCATION: (668)
US-09-464-535-31
```

```
Query Match      61.3%; Score 19; DB 3; Length 673;
Best Local Similarity 81.5%; Pred. No. 42;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      5 CCACCGGAGTTGAGTAGACGGTCTG 31
DB      362 CCACCGGAGTTGAGTAGACCGGTGTG 336
```

RESULT 9

```
US-09-351-224E-7/c
Sequence 7, Application US/09351224E
Patent No. 6388171
GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Craesta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224E
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1578
TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: permease, fully spliced cDNA
US-09-351-224E-7
```

```
Query Match      61.3%; Score 19; DB 3; Length 1578;
Best Local Similarity 81.5%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      4 GCCACCGGAGTTGAGTAGACGGTCTG 30
DB      321 GCCACCGGAGTTGAGTAGACCGTGTG 295
```

RESULT 10

```
US-09-677-488A-7/c
Sequence 7, Application US/09677488A
Patent No. 6482621
GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Craesta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 35718/204100
CURRENT APPLICATION NUMBER: US/09/677,488A
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
```

```
LENGTH: 1578
TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: permease, fully spliced cDNA
US-09-677-488A-7
```

```
Query Match      61.3%; Score 19; DB 3; Length 1578;
Best Local Similarity 81.5%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      4 GCCACCGGAGTTGAGTAGACGGTCTG 30
DB      321 GCCACCGGAGTTGAGTAGACCGTGTG 295
```

RESULT 11

```
US-09-677-682B-7/c
Sequence 7, Application US/09677682B
Patent No. 6534291
GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Craesta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,682B
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1578
TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: permease, fully spliced cDNA
US-09-677-682B-7
```

```
Query Match      61.3%; Score 19; DB 3; Length 1578;
Best Local Similarity 81.5%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      4 GCCACCGGAGTTGAGTAGACGGTCTG 30
DB      321 GCCACCGGAGTTGAGTAGACCGTGTG 295
```

RESULT 12

```
US-09-882-694B-7/c
Sequence 7, Application US/09882694B
Patent No. 6822140
GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Craesta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 35718/208255
CURRENT APPLICATION NUMBER: US/09/882,694B
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
```

```
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1578)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permease, fully spliced cDNA
US-09-882-694B-7
```

```
Query Match          61.3%; Score 19; DB 3; Length 1578;
Best Local Similarity 81.5%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      4 GCCACCGGAGTTGAGTAGACGGTGCT 30
Db      321 GCCACCGGAGTCGGGTAGACGCTGCT 295
```

```
RESULT 13
US-09-351-224E-6/c
; Sequence 6, Application US/09351224E
; Patent No. 6388171
; GENERAL INFORMATION:
; APPLICANT: Duviak, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Craeta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; FILE REFERENCE: 5718-111
; CURRENT APPLICATION NUMBER: US/09/351,224E
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permease, partially spliced cDNA
US-09-351-224E-6
```

```
Query Match          61.3%; Score 19; DB 3; Length 1764;
Best Local Similarity 81.5%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      4 GCCACCGGAGTTGAGTAGACGGTGCT 30
Db      325 GCCACCGGAGTCGGGTAGACGCTGCT 299
```

```
RESULT 14
US-09-677-488A-6/c
; Sequence 6, Application US/09677488A
; Patent No. 6482621
; GENERAL INFORMATION:
; APPLICANT: Duviak, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Craeta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; FILE REFERENCE: 35718/204100
```

```
; CURRENT APPLICATION NUMBER: US/09/677,488A
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permease, partially spliced cDNA
US-09-677-488A-6
```

```
Query Match          61.3%; Score 19; DB 3; Length 1764;
Best Local Similarity 81.5%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      4 GCCACCGGAGTTGAGTAGACGGTGCT 30
Db      325 GCCACCGGAGTCGGGTAGACGCTGCT 299
```

```
RESULT 15
US-09-677-682B-6/c
; Sequence 6, Application US/09677682B
; Patent No. 6534291
; GENERAL INFORMATION:
; APPLICANT: Duviak, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Craeta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; FILE REFERENCE: 35718/204101
; CURRENT APPLICATION NUMBER: US/09/677,682B
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permease, partially spliced cDNA
US-09-677-682B-6
```

```
Query Match          61.3%; Score 19; DB 3; Length 1764;
Best Local Similarity 81.5%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      4 GCCACCGGAGTTGAGTAGACGGTGCT 30
Db      325 GCCACCGGAGTCGGGTAGACGCTGCT 299
```

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OM nucleic - nucleic search, using sw model

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651.599 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31

Sequence: 1 tcgcacccggaagtgtgtagacggtgctg 31

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	31	8	US-10-688-489-59
2	30	96.8	10945	7	US-10-361-002-5
3	30	96.8	10945	7	US-10-361-004-5
4	30	96.8	10975	8	US-10-699-550-1
5	30	96.8	11029	8	US-10-699-550-2
6	30	96.8	11029	8	US-10-679-520A-66
7	30	96.8	11029	9	US-10-706-892-1
8	30	96.8	11029	9	US-10-706-892-2
9	30	96.8	11029	9	US-10-985-805-1
10	30	96.8	11029	9	US-10-956-085-1
11	22	71.0	22	8	US-10-688-489-68
12	21	67.7	21	8	US-10-688-489-63
13	21	67.7	21	8	US-10-688-489-67
14	21	67.7	21	8	US-10-688-489-70
15	20.6	66.5	21	10	US-11-110-517-1
16	20.6	66.5	43	5	US-10-196-723A-32
17	20.6	66.5	590	4	US-09-925-065A-446157
18	20.6	66.5	590	4	US-09-925-065A-446158
c 19	20.6	66.5	1517	9	US-10-964-195-12
c 20	20.6	66.5	1517	9	US-10-964-195-10
c 21	20.6	66.5	1527	6	US-10-074-596-10
22	20.4	65.8	612	4	US-09-925-065A-854826
23	20	64.5	20	8	US-10-688-489-62

ALIGNMENTS

RESULT 1

US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Paul M.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.0T
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 31
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-59

Query Match 100.0%; Score 31; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2

US-10-361-002-5
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gilmeister, Lidja

Sequence 69, Appl
Sequence 71, Appl
Sequence 52, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 38, Appl
Sequence 29, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 9300, Ap
Sequence 6914, Ap
Sequence 7527, Ap
Sequence 103171,
Sequence 103172,
Sequence 103171,
Sequence 103172,
Sequence 69, Appl
Sequence 35048, A
Sequence 35047, A
Sequence 356395,

```
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match          96.8%; Score 30; DB 7; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
        ||||||||||||||||||||||||||||
Db      10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 3
US-10-361-004-5
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gilmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match          96.8%; Score 30; DB 7; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
        ||||||||||||||||||||||||||||
Db      10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510

RESULT 4
US-10-699-550-1
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: 60/402,860
; CURRENT FILING DATE: 2002-08-08
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; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match          96.8%; Score 30; DB 8; Length 10975;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
        ||||||||||||||||||||||||||||
Db      10505 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10534

RESULT 5
US-10-699-550-2
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match          96.8%; Score 30; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
        ||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 6
US-10-679-520A-66
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; CURRENT FILING DATE: 2003-10-06
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;
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: FR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match 96.8%; Score 30; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 7
US-10-706-892-1
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-1

Query Match 96.8%; Score 30; DB 9; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 8
US-10-706-892-2
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
; FILE REFERENCE: 454311-2231.1
; CURRENT APPLICATION NUMBER: US/10/706,892
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,117
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 3.2

;
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-706-892-2

Query Match 96.8%; Score 30; DB 9; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 9
US-10-985-805-1
; Sequence 1, Application US/10985805
; Publication No. US20050130133A1
; GENERAL INFORMATION:
; APPLICANT: Burde, Stefan H.M.
; APPLICANT: Gierman, Todd M.
; APPLICANT: Glenn, Christopher C.
; TITLE OF INVENTION: Oligonucleotides and Methods for Detection of West Nile Virus
; FILE REFERENCE: 7430*201
; CURRENT APPLICATION NUMBER: US/10/985,805
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/519,096
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: West Nile virus consensus sequence
US-10-985-805-1

Query Match 96.8%; Score 30; DB 9; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|||||
Db 10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552

RESULT 10
US-10-956-085-1
; Sequence 1, Application US/10956085
; Publication No. US20050164170A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, PHILIPPE
; APPLICANT: DEUBEL, VINCENT
; APPLICANT: GUENET, JEAN-LOUIS
; APPLICANT: DROUET, MARIE-THERESE
; APPLICANT: MALKINSON, MERTYN
; APPLICANT: BANET, CAROLINE
; APPLICANT: FRENKIEL, MARIE-PASCALE
; APPLICANT: COURAGEOT, MARIE-PIERRE
; APPLICANT: COULIBALY, FASSELI
; APPLICANT: CATTEAU, ADELINE
; APPLICANT: FLAMAND, MARIE
; TITLE OF INVENTION: NEUROVIRULENT STRAIN OF THE WEST NILE VIRUS AND APPLICATIONS
; FILE REFERENCE: 243477USOXPCT
; CURRENT APPLICATION NUMBER: US/10/956,085
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01168
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: FR01/04599
; PRIOR FILING DATE: 2001-04-04

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; PRIOR APPLICATION NUMBER: FR01/11525
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: Flavivirus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-956-085-1

Query Match      96.8%; Score 30; DB 9; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CCGCCACCGGAGTTGAGTAGACGGTGCTG 31
Db      10523 CCGCCACCGGAGTTGAGTAGACGGTGCTG 10552

RESULT 11
US-10-688-489-68
; Sequence 68, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 44
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-68

Query Match      71.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10  GGAAGTTGAGTAGACGGTGCTG 31
Db      1  GGAAGTTGAGTAGACGGTGCTG 22

RESULT 12
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63

Query Match      67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TCCGCCACCGGAGTTGAGTA 21
Db      1  TCCGCCACCGGAGTTGAGTA 21

RESULT 13
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-67

Query Match      67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10  GGAAGTTGAGTAGACGGTGCT 30
Db      1  GGAAGTTGAGTAGACGGTGCT 21

RESULT 14
US-10-688-489-70
; Sequence 70, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Wu, Wen
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63
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; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-70

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```

Query Match 67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 11 GAAGTTGAGTAGACGGTGCTG 31
DB 1 GAAGTTGAGTAGACGGTGCTG 21

```

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RESULT 15
US-11-110-517-1
; Sequence 1, Application US/11110517
; Publication NO. US20050186222A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: UytdeHaag, Alphonsus GCM
; APPLICANT: Goudemits, Jaap
; APPLICANT: Schouten, Govert J
; TITLE OF INVENTION: Vaccine against West Nile virus
; FILE REFERENCE: 0082W00000RD
; CURRENT APPLICATION NUMBER: US/11/110,517
; CURRENT FILING DATE: 2005-04-20
; PRIOR APPLICATION NUMBER: PCT/NL02/00718
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/EP03/50129
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide WNV 1
US-11-110-517-1

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Query Match 66.5%; Score 20.6; DB 10; Length 21;
Best Local Similarity 95.2%; Pred. No. 16;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 5 CCACCGGAAGTTGAGTAGACG 25
DB 1 CCACCGGAGTTGAGTAGACG 21

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Job time : 394.418 secs

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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 04:19:53 ; Search time 1697 Seconds
(without alignments)
1038.390 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcaccggaagttgtagtagcgggtgtg 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

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Total number of hits satisfying chosen parameters: 1209584

Minimum DB seq length: 18
Maximum DB seq length: 31

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	12	38.7	20	6	AX350865 Sequence
c 3	12	38.7	21	6	CQ815914 Sequence
c 4	11	35.5	19	6	AX429360 Sequence
c 5	11	35.5	20	6	BD089943 A method
c 6	11	35.5	21	6	CS014127 Sequence
c 7	11	35.5	21	6	AX676187 Sequence
c 8	11	35.5	22	6	AR649551 Sequence
c 9	11	35.5	23	6	BD176902 Gene enco
c 10	11	35.5	23	6	BD266802 Methods f
c 11	11	35.5	23	6	AX587376 Sequence
c 12	11	35.5	24	6	E07234 Primer. 9/1
c 13	11	35.5	24	6	I32494 Sequence 14
c 14	11	35.5	24	6	I43439 Sequence 14
c 15	11	35.5	24	6	AR181929 Sequence
c 16	11	35.5	24	6	AR494625 Sequence
c 17	11	35.5	24	6	AR656106 Sequence
c 18	11	35.5	24	6	AX445342 Sequence

19 11 35.5 24 6 AX494089 Sequence
20 11 35.5 25 6 AR137232 Sequence
21 11 35.5 25 6 AR156944 Sequence
c 22 11 35.5 25 6 AR350223 Sequence
c 23 11 35.5 25 6 AX354290 Sequence
c 24 11 35.5 29 6 AX192031 Sequence
c 25 11 35.5 31 6 AR656122 Sequence
c 26 11 35.5 31 6 AR656136 Sequence
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44 10 32.3 19 6 E06911 Synthetic D
45 10 32.3 19 6 I27509 Sequence 23

ALIGNMENTS

RESULT 1
AX045081/c
LOCUS AX045081 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 11 from Patent WO0066149.
ACCESSION AX045081
VERSION AX045081.1 GI:11343680
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gerhardt, C., Romero-Romero, I.A. and Strosberg, A.D.
TITLE Medicines useful for treating disorders of regulation of body
fatness and diseases related to disorders of leptin production
JOURNAL Patent: WO 0066149-A 11 09-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (FR)
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QY 16 TGAGTAGACGGT 27
18 TGAGTAGACGGT 7
Db
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AX350865
LOCUS AX350865 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0183816.
ACCESSION AX350865
VERSION AX350865.1 GI:18616322
KEYWORDS synthetic construct
SOURCE synthetic construct

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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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source
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  Neri,D. and Viti,F.
  Method for detecting tumors
  Patent: WO 013816-A 5 08-NOV-2001;
  Phillogen S.R.L. (IT)
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LOCUS      CQ815914                21 bp    DNA    linear    PAT 03-JUN-2004
DEFINITION Sequence 1 from Patent WO2004042042.
ACCESSION  CQ815914
VERSION     CQ815914.1 GI:48144439
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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RESULT 4
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LOCUS      AX429360                19 bp    DNA    linear    PAT 21-JUN-2002
DEFINITION Sequence 6 from Patent WO0234953.
ACCESSION  AX429360
VERSION     AX429360.1 GI:21540661
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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  Reynolds,T.R.
  Detection and quantification of human herpes viruses
  Patent: WO 0234953-A 6 02-MAY-2002;
  HARRIS, ROBERT B (US)
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Db       16 AGACGGTCTG 6

RESULT 5
BD089943/c
LOCUS      BD089943                20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION  BD089943
VERSION     BD089943.1 GI:22635553
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2001321190-A/2187
PD 20-NOV-2001
PI 12-MAR-2001 JP 2001068285
PF EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,PC
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PC C12N15/00
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RESULT 6
CS014127/c
LOCUS      CS014127                21 bp    DNA    linear    PAT 11-FEB-2005
DEFINITION Sequence 4052 from Patent WO2005007144.
ACCESSION  CS014127
VERSION     CS014127.1 GI:59673942
KEYWORDS
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE
AUTHORS
Hakonarson,H., Gurney,M.E. and Halapi,E.
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TITLE Methods of diagnosis and treatment for asthma based on haplotype association
JOURNAL Patent: WO 2005007144-A 4052 27-JAN-2005;
Decode Genetics EHP. (IS)
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QY 11 GAAGTTGAGTA 21
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Db 19 GAAGTTGAGTA 9
RESULT 7
AX676187 21 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 44 from Patent WO02057429.
ACCESSION AX676187
VERSION AX676187.1 GI:29333863
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Yan, W.L.
TITLE A method for producing a population of homozygous stem cells having a pre-selected immunophenotype and/or genotype
JOURNAL Patent: WO 02057429-A 44 25-JUL-2002;
Stemtron, Inc. (US)
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Db 4 GAAGTTGAGTA 14
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AR649551/c
LOCUS
DEFINITION Sequence 20 from patent US 6875757.
ACCESSION AR649551
VERSION AR649551.1 GI:62792791
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Miller, D.D., Tigay, G., Dalton, J.T., Sardar, V.M., Elrod, D.B., Xu, H., Baker, D.L., Wang, D., Lilliom, K., Fischer, D.J., Virag, T. and Nusser, N.
TITLE LPA receptor agonists and antagonists and methods of use
JOURNAL Patent: US 6875757-A 20 05-APR-2005;
University of Tennessee Research Foundation; Knoxville, TN
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ORIGIN
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QY 21 AGACGGTGCTG 31
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Db 17 AGACGGTGCTG 7
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BD176902/c
LOCUS
DEFINITION Gene encoding an amino acid sequence relating to cytokinin synthesis.
ACCESSION BD176902
VERSION BD176902.1 GI:29122830
KEYWORDS WO 02072818-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kakimoto, T. and Sakakibara, H.
TITLE Gene encoding an amino acid sequence relating to cytokinin synthesis
JOURNAL Patent: WO 02072818-A 22 19-SEP-2002;
SUNTORY LTD, NIPPON PAPER INDUSTRIES CO LTD, TATSUO KAKIMOTO, HITOSHI SAKAKIBARA
COMMENT OS Artificial Sequence
PN WO 02072818-A/22
PD 19-SEP-2002
PF 12-MAR-2002 WO 2002JP002315
PR 12-MAR-2001 JP 01P 069489
PI TATSUO KAKIMOTO, HITOSHI SAKAKIBARA
PC C12N15/09, C12N9/14, C12N9/10, C12Q1/68, A01H5/00 CC Primer 918
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Db 19 GGAAGTTGAGT 9
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LOCUS
DEFINITION Methods for treating cancer and for mediating chemotaxis of dendritic cells.
ACCESSION BD266802
VERSION BD266802.1 GI:33076570
KEYWORDS JP 2002533402-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Keting, C., Xin, H., Chan, V.W.F., Kothakota, S., Williams, L.T. and Winter, J.A.
TITLE Methods for treating cancer and for mediating chemotaxis of dendritic cells
JOURNAL Patent: JP 2002533402-A 22 08-OCT-2002;

CHIRON CORP
OS Artificial Sequence
PN JP 2002533402-A/22
PD 08-OCT-2002
PF 28-DEC-1999 JP 2000590657
PR 31-DEC-1998 US 60/114498
PI CHU KETING,HONG XIN,VIVIEN F F CHAN,SRINIVAS
KOTHAKOTA,LEWIS T
PI WILLIAMS,
PI JILL A WINTER
PC
A61K38/00,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
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QY 17 GAGTAGACGGT 27
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AX587376/c
LOCUS AX587376 23 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 152 from Patent WO0236761.
ACCESSION AX587376
VERSION AX587376.1 GI:27656241
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
TITLE Methods and compositions for the diagnosis of cancer
susceptibilities and defective dna repair mechanisms and treatment
thereof
JOURNAL Patent: WO 0236761-A 152 10-MAY-2002;
DANA FARBER CANCER INSTITUTE (US)
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QY 10 GGAAGTTGAGT 20
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Db 13 GGAAGTTGAGT 3

RESULT 12
E07234/c
LOCUS E07234 24 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer.
ACCESSION E07234

VERSION E07234.1 GI:2175375
KEYWORDS JP 1994100594-A/10.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Okuno,Y., Isekawa,Y., Sasao,F. and Ueda,S.
TITLE ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
JOURNAL Patent: JP 1994100594-A 10 12-APR-1994;
TAKARA SHUZO CO LTD

COMMENT
OS None
OC Artificial sequences.
PN JP 1994100594-A/10
PD 12-APR-1994
PF 17-SEP-1992 JP 1992272538
PI OKUNO YOSHINOBU, ISEKAWA YUJI, SASAO FUYOKO, UEDA SHIGEHARU PC
C07K13/00,A61K39/00,A61K39/00,A61K39/395,A61K39/395,C12N15/44, PC
C12P21/02,

PC
C12P21/08,G01N33/53,G01N33/569,(C12P21/02,C12R1:91),(C12P21/08, PC
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CC topology: Linear;
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QY 13 AGTTGAGTAGA 23
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Db 12 AGTTGAGTAGA 2

RESULT 13
I32494/c
LOCUS I32494 24 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 14 from patent US 5589174.
ACCESSION I32494
VERSION I32494.1 GI:1823285
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5589174-A 14 31-DEC-1996;
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ORIGIN

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Db 12 AGTTGAGTAGA 2

RESULT 14

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LOCUS       I43439               24 bp      DNA          linear      PAT 07-OCT-1997
DEFINITION   Sequence 14 from patent US 5631350.
ACCESSION   I43439
VERSION     I43439.1  GI:2468683
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 24)
AUTHORS     Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE       Anti-human influenza virus antibody
JOURNAL     Patent: US 5631350-A 14 20-MAY-1997;
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
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Db       12 AGTTGAGTAGA 2

RESULT 15
AR181929/c
LOCUS       AR181929             24 bp      DNA          linear      PAT 20-APR-2002
DEFINITION   Sequence 14 from patent US 6337070.
ACCESSION   AR181929
VERSION     AR181929.1  GI:20224845
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 24)
AUTHORS     Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE       Polypeptides for use in generating anti-human influenza virus
             antibodies
JOURNAL     Patent: US 6337070-A 14 08-JAN-2002;
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QY      13 AGTTGAGTAGA 23
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GenCore version 5.1.6
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SUMMARIES

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13	18	58.1	19	ADN36739	Adn36739 West Nile
14	18	58.1	26	ADN36825	Adn36825 West Nile
15	17	54.8	18	ADN36743	Adn36743 West Nile
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c	25	12	38.7	18	12	ADN36859	Adn36859 West Nile
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c	27	12	38.7	20	4	AAC84110	Aac84110 Human alp
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c	29	12	38.7	21	12	ADO21519	Ado21519 West Nile
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c	40	11	35.5	19	6	ABA01459	Abao1459 Streptoco
c	41	11	35.5	20	2	AAQ26927	Aaq26927 Biotinyia
c	42	11	35.5	20	6	ABU45143	Abi45143 Human chr
c	43	11	35.5	20	6	ABK27391	Abk27391 Gamma-ami
c	44	11	35.5	20	12	ADG65356	Adg65356 S1P-4 ant
c	45	11	35.5	20	12	ADG65384	Adg65384 Edg-6 ant

ALIGNMENTS

RESULT 1
ADN36737
ID ADN36737 standard; DNA; 31 BP.
XX
AC ADN36737;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID59.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
(GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 18; SEQ ID NO 59; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be

CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

XX
SQ Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 31; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
DB 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2

ADN36746

ID ADN36746 standard; DNA; 22 BP.

XX
AC ADN36746;

XX
DT 15-JUL-2004 (first entry)

XX
DE West Nile virus detection-related PCR primer SeqID68.

XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.

XX
OS West Nile virus.

XX
PN WO2004036190-A2.

XX
PD 29-APR-2004.

XX
PF 10-OCT-2003; 2003WO-US033639.

XX
PR 16-OCT-2002; 2002US-0418891P.

XX
PR 25-NOV-2002; 2002US-0429006P.

XX
PR 24-FEB-2003; 2003US-0449810P.

XX
PA (GENP-) GEN-PROBE INC.

XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX
DR WPI; 2004-389590/36.

XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX
PS Claim 26; SEQ ID NO 68; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.

XX

SQ Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAGACGGTGCTG 31
DB 1 GGAAGTTGAGTAGACGGTGCTG 22

RESULT 3

ADN36741

ID ADN36741 standard; DNA; 21 BP.

XX
AC ADN36741;

XX
DT 15-JUL-2004 (first entry)

XX
DE West Nile virus detection-related oligonucleotide probe SeqID63.

XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.

XX
OS West Nile virus.

XX
PN WO2004036190-A2.

XX
PD 29-APR-2004.

XX
PF 10-OCT-2003; 2003WO-US033639.

XX
PR 16-OCT-2002; 2002US-0418891P.

XX
PR 25-NOV-2002; 2002US-0429006P.

XX
PR 24-FEB-2003; 2003US-0449810P.

XX
PA (GENP-) GEN-PROBE INC.

XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX
DR WPI; 2004-389590/36.

XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX
PS Claim 26; SEQ ID NO 63; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAGTA 21
DB 1 TCCGCCACCGGAAGTTGAGTA 21

```

RESULT 4
ADN36745
ID ADN36745 standard; DNA; 21 BP.
XX
AC ADN36745;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related PCR primer SeqID67.
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
XX WO2004036190-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
XX
XX 25-NOV-2002; 2002US-0429006P.
XX
XX 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX
XX Claim 26; SEQ ID NO 67; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
XX Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
SQ
Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GGAAGTTGAGTACACGGTGCT 30
Db 1 GGAAGTTGAGTACACGGTGCT 21
XX
RESULT 5
ADN36748
ID ADN36748 standard; DNA; 21 BP.
XX
XX
AC ADN36748;
XX
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related PCR primer SeqID70.
DE

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XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
XX WO2004036190-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-US033639.
XX
XX 16-OCT-2002; 2002US-0418891P.
XX
XX 25-NOV-2002; 2002US-0429006P.
XX
XX 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX
XX Claim 26; SEQ ID NO 70; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
XX Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
SQ
Query Match 67.7%; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGAAGTTGAGTACACGGTGCTG 31
Db 1 GGAAGTTGAGTACACGGTGCTG 21
XX
RESULT 6
ADN36749
ID ADN36749 standard; DNA; 20 BP.
XX
AC ADN36749;
XX
XX 15-JUL-2004 (first entry)
XX
XX West Nile virus detection-related PCR primer SeqID71.
XX
XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
XX WO2004036190-A2.
XX

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PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 71; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of a PCR primer which is related to the
XX invention.
XX
XX Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 64.5%; Score 20; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.091;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 12 AAGTTGAGTAGACGGTGCTG 31
XX |||||||
XX Db 1 AAGTTGAGTAGACGGTGCTG 20
XX
XX RESULT 7
XX ADN36740
XX ID ADN36740 standard; DNA; 20 BP.
XX AC ADN36740;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE West Nile virus detection-related oligonucleotide probe SeqID62.
XX
XX KW hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; probe; ss.
XX
XX OS West Nile virus.
XX
XX PN WO2004036190-A2.
XX
XX PD 29-APR-2004.
XX
XX PF 10-OCT-2003; 2003WO-US033639.
XX
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 69; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of a PCR primer which is related to the
XX invention.
XX
XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 64.5%; Score 20; DB 12; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.091;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TCCGCCACCGAAGTTGAGT 20
XX |||||||
XX Db 1 TCCGCCACCGAAGTTGAGT 20
XX
XX RESULT 8
XX ADN36747
XX ID ADN36747 standard; DNA; 20 BP.
XX AC ADN36747;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE West Nile virus detection-related PCR primer SeqID69.
XX
XX KW hybridisation assay probe; nucleic acid detection;
XX target-complementary sequence; flavivirus; West Nile virus; WNV;
XX RNA virus; infection; meningitis; encephalitis;
XX high throughput screening; PCR; primer; ss.
XX
XX OS West Nile virus.
XX
XX PN WO2004036190-A2.
XX
XX PD 29-APR-2004.
XX
XX PF 10-OCT-2003; 2003WO-US033639.
XX
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX WPI; 2004-389590/36.
XX
XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
PT
XX Claim 26; SEQ ID NO 69; 135pp; English.
XX
XX This invention relates to a novel hybridisation assay probe, for
```

CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.

XX Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
SQ
Query Match 64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
DB 1 GAAGTTGAGTAGACGGTGCT 20
|||||

RESULT 9
ID AEA35007
AC AEA35007 standard; DNA; 20 BP.

XX AEA35007;

XX 28-JUL-2005 (first entry)

XX West Nile virus consensus genome-derived PCR primer, SEQ ID NO:52.

XX Microorganism detection; diagnosis; West Nile virus infection; infection;
KW neurological disease; PCR; primer; ss.

XX West Nile virus; strain NY99-flamingo382-99.
OS West Nile virus; strain NY99-eghs.
OS West Nile virus; strain HNY1999.
OS West Nile virus; isolate 2741.
OS West Nile virus; isolate WN MD 2000-crow265.
OS West Nile virus; isolate WN NJ 2000 MQ5488.
OS West Nile virus; isolate WN NY 2000-grouse3282.
OS West Nile virus; isolate WN NY 2000-crow3356.
XX
PN WO2005047522-A2.

XX 26-MAY-2005.

XX 10-NOV-2004; 2004WO-US037558.

XX 12-NOV-2003; 2003US-0519096P.

XX (FARB) BAYER HEALTHCARE LLC.

XX Burde SHM, Gierman TM, Glenn CC;

XX WPI; 2005-372389/38.

XX Isolated oligonucleotide for detecting West Nile virus, comprises
PT oligonucleotide sequences.

XX Claim 1; SEQ ID NO 52; 65pp; English.

XX The invention relates to oligonucleotide primers and probes (AEA34957-
CC AEA35014) derived from a West Nile virus consensus sequence (AEA34956).
CC The invention also relates to a method of detecting West Nile virus in a
CC test sample (especially human blood plasma), a test kit comprising one or
CC more oligonucleotides of the invention, and a method for identifying
CC primers for the detection of a nucleic acid sequence. Although West Nile
CC virus rarely kills, about one in 150 people who become infected develop a
CC potentially deadly case of encephalitis or meningitis, and there is

CC currently no means of treatment or prevention of West Nile virus
CC infection. The primers, probes, methods and kits are useful for the
CC effective and early detection of West Nile virus infection, facilitating
CC the diagnosis of infection and the appropriate treatment of symptoms.
CC Sequences AEA34957-AEA35008 represent oligonucleotide primers suitable
CC for use in PCR amplification which are derived from the West Nile virus
CC consensus sequence referred to in the invention (AEA34956).

XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAGTAGA 23
DB 1 GCCACCGGAAGTTGAGTAGA 20
|||||

RESULT 10
ADN36744

ID ADN36744 standard; DNA; 19 BP.

XX ADN36744;

XX 15-JUL-2004 (first entry)

XX West Nile virus detection-related oligonucleotide probe SeqID66.

XX hybridisation assay probe; nucleic acid detection;

KW target-complementary sequence; flavivirus; West Nile virus; WNV;

KW RNA virus; infection; meningitis; encephalitis;

KW high throughput screening; probe; ss.

XX West Nile virus.

XX WO2004036190-A2.

XX 29-APR-2004.

XX 10-OCT-2003; 2003WO-US033639.

XX 16-OCT-2002; 2002US-0418891P.

XX 25-NOV-2002; 2002US-0429006P.

XX 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.

XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.

XX Claim 26; SEQ ID NO 66; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

XX Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

```
Query Match      61.3%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGAGTA 21
DB 1 CGCCACCGGAAGTTGAGTA 19

RESULT 11
ADN36738
ID ADN36738 standard; DNA; 19 BP.
XX
AC ADN36738;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID60.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 60; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      61.3%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
DB 1 TCCGCCACCGGAAGTTGAG 19

RESULT 12
ADN36739
ID ADN36739 standard; DNA; 19 BP.
XX
AC ADN36739;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID61.
XX
KW hybridisation assay probe; nucleic acid detection;
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ADN36742
ID ADN36742 standard; DNA; 18 BP.
XX
AC ADN36742;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related PCR primer SeqID64.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 64; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      58.1%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGAGT 20
DB 1 CGCCACCGGAAGTTGAGT 18

RESULT 13
ADN36739
ID ADN36739 standard; DNA; 19 BP.
XX
AC ADN36739;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID61.
XX
KW hybridisation assay probe; nucleic acid detection;
```

KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX West Nile virus.

XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= i

XX WO2004036190-A2.

XX 29-APR-2004.

XX 10-OCT-2003; 2003WO-US033639.

XX 16-OCT-2002; 2002US-0418891P.

XX 25-NOV-2002; 2002US-0429006P.

XX 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.

XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX New hybridization assay probe comprising target-complementary sequence of

XX bases, useful in detecting flavivirus, e.g. West Nile virus.

XX Disclosure; SEQ ID NO 61; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

XX SQ Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 58.1%; Score 18; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGGAGCTTGAG 19

Db 2 CCGCCACCGGAGCTTGAG 19

RESULT 14

ADN36825/c

ID ADN36825 standard; RNA; 26 BP.

XX AC ADN36825;

XX 15-JUL-2004 (first entry)

XX West Nile virus detection-related oligonucleotide probe SeqID147.

XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.

XX West Nile virus.

XX Key Location/Qualifiers
FH modified_base 1..26
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"

XX WO2004036190-A2.

XX 29-APR-2004.

XX 10-OCT-2003; 2003WO-US033639.

XX 16-OCT-2002; 2002US-0418891P.

XX 25-NOV-2002; 2002US-0429006P.

XX 24-FEB-2003; 2003US-0449810P.

XX (GENP-) GEN-PROBE INC.

XX Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX WPI; 2004-389590/36.

XX New hybridization assay probe comprising target-complementary sequence of

XX bases, useful in detecting flavivirus, e.g. West Nile virus.

XX Example 1; SEQ ID NO 147; 135pp; English.

XX This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

XX SQ Sequence 26 BP; 6 A; 10 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 58.1%; Score 18; DB 12; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCTG 31

Db 26 GTTGAGTAGACGGTGCTG 9

RESULT 15

ADN36743

ID ADN36743 standard; DNA; 18 BP.

XX AC ADN36743;

XX 15-JUL-2004 (first entry)

XX West Nile virus detection-related oligonucleotide probe SeqID65.

XX hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.

XX West Nile virus.

XX Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

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FT XX /mod_base= i
XX PN WO2004036190-A2.
XX XX
XX PD 29-APR-2004.
XX XX
XX PF 10-OCT-2003; 2003WO-US033639.
XX XX
XX PR 16-OCT-2002; 2002US-0418891P.
XX PR 25-NOV-2002; 2002US-0429006P.
XX PR 24-FEB-2003; 2003US-0449810P.
XX XX
XX PA (GENP-) GEN-PROBE INC.
XX XX
XX FI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX DR
XX DR WPI; 2004-389590/36.
XX XX
XX PT New hybridization assay probe comprising target-complementary sequence of
XX PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX PS
XX PS Claim 26; SEQ ID NO 65; 135pp; English.
XX CC
XX CC This invention relates to a novel hybridisation assay probe, for
XX CC detecting a nucleic acid, which is a probe sequence that comprises a
XX CC target-complementary sequence of bases, and optionally one or more base
XX CC sequences that are not complementary to the nucleic acid that is to be
XX CC detected. The hybridisation assay probes and the kits are useful in
XX CC detecting and amplifying a target nucleic acid sequence, for example
XX CC flavivirus like West Nile virus, that may be present in a biological
XX CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX CC birds and culex mosquitoes, with humans and horses serving as incidental
XX CC hosts. Infection of humans can lead to meningitis or encephalitis. The
XX CC invention may allow for accurate and efficient high throughput screening.
XX CC The present sequence is that of an oligonucleotide probe which is related
XX CC to the invention.
XX SQ
XX SQ Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;

Query March 54.8%; Score 17; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 4 GCCACCGGAAGTTGAGT 20
   |||||
Db 2 GCCACCGGAAGTTGAGT 18
   |||||

Search completed: December 12, 2005, 04:38:26
Job time : 270 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 04:20:28 ; Search time 1949 Seconds
(without alignments)
744.176 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcacccgaagttagtagacgtgtgctg 31

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0
Total number of hits satisfying chosen parameters: 52288

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hc:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_gsa1:*
- 10: gb_gsa2:*
- 11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	38.7	27	1 AJ689351	AJ689351
C 2	10	32.3	27	5 BQ540272	BQ540272 PTAM0589
C 3	10	32.3	27	8 DN955493	DN955493 it88e12.g
C 4	10	32.3	29	10 C2473162	C2473162 d03077-3p
C 5	10	32.3	31	3 BM395985	BM395985 5009-0-15
C 6	9	29.0	18	3 BM397227	BM397227 5009-0-3-
C 7	9	29.0	18	3 BM400126	BM400126 5009-0-66
C 8	9	29.0	19	3 BM397047	BM397047 5009-0-28
C 9	9	29.0	19	3 BM397791	BM397791 5009-0-37
C 10	9	29.0	19	3 BM398839	BM398839 5009-0-5-
C 11	9	29.0	19	3 BM398882	BM398882 5009-0-50
C 12	9	29.0	20	1 AJ685250	AJ685250
C 13	9	29.0	20	3 BM397370	BM397370 5009-0-31
C 14	9	29.0	20	3 BM398074	BM398074 5009-0-40
C 15	9	29.0	20	3 BM398469	BM398469 5009-0-45
C 16	9	29.0	20	10 AJ587566	AJ587566 Arabidops
C 17	9	29.0	21	1 AJ681837	AJ681837
C 18	9	29.0	21	3 BM398235	BM398235 5009-0-42
C 19	9	29.0	21	3 BM400058	BM400058 5009-0-65
C 20	9	29.0	21	3 BM400084	BM400084 5009-0-8-
C 21	9	29.0	21	3 BM401072	BM401072 5009-0-82
C 22	9	29.0	21	9 AZ774560	AZ774560 2M0004H08

C 23	9	29.0	22	1 AJ651078	AJ651078
C 24	9	29.0	22	3 BM395131	BM395131 50072-2-7
C 25	9	29.0	22	3 BM397203	BM397203 5009-0-3-
C 26	9	29.0	22	3 BM398652	BM398652 5009-0-48
C 27	9	29.0	22	3 BM399045	BM399045 5009-0-52
C 28	9	29.0	22	3 BM399148	BM399148 5009-0-54
C 29	9	29.0	22	3 BM400176	BM400176 5009-0-68
C 30	9	29.0	22	3 BM400906	BM400906 5009-0-80
C 31	9	29.0	22	3 BM401082	BM401082 5009-0-82
C 32	9	29.0	22	3 BM401155	BM401155 5009-0-83
C 33	9	29.0	22	8 DR908038	DR908038 CCSEN06F0
C 34	9	29.0	22	11 TA259H01Q	AL488407 T. brucei
C 35	9	29.0	23	3 BM395136	BM395136 50072-2-7
C 36	9	29.0	23	3 BM395635	BM395635 5009-0-1-
C 37	9	29.0	23	3 BM396314	BM396314 5009-0-2-
C 38	9	29.0	23	3 BM397693	BM397693 5009-0-35
C 39	9	29.0	23	3 BM399213	BM399213 5009-0-55
C 40	9	29.0	23	3 BM399677	BM399677 5009-0-6-
C 41	9	29.0	23	3 BM401179	BM401179 5009-0-83
C 42	9	29.0	23	9 AZ324328	AZ324328 IM0046B16
C 43	9	29.0	23	9 AZ647047	AZ647047 IM0513B22
C 44	9	29.0	23	11 TA66H11P	AL458350 T. brucei
C 45	9	29.0	24	3 BM396768	BM396768 5009-0-25

ALIGNMENTS

RESULT 1
AJ689351/c
LOCUS AJ689351 27 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ689351 KN261 Bos taurus CDNA clone KN261-050_N13, mRNA sequence.
ACCESSION AJ689351
VERSION AJ689351.1 GI:49421959
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 27)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: SmaI 3' Seq Primer M13F Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..27
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-050_N13"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

FEATURES
source
1..27
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-050_N13"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

ORIGIN

Query Match 38.7%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2

/clone lib="Exelixis P element XP insertions"
 /note="Vector: P element XP (GenBank accession number
 AY151149); An isogenic w- Drosophila melanogaster strain
 was mutagenized by remobilization of transposable
 elements. For the P element XP, we selected an easily
 mobilized ammunition element among inserts hopped onto the
 Binsyncy balancer. New insertions were collected in vials
 from dysgenic females using the standard chromosomal
 source of transposase, delta2-3. All lines were mapped to
 a chromosome by standard genetic methods, examined for
 homozygous viability and used for recovery of flanking
 genomic sequence by inverse PCR."

ORIGIN

Query Match 32.3%; Score 10; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.6e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GTAGACGGTG 28
 |||||
 Db 14 GTAGACGGTG 5

RESULT 5

BM395985/c
 LOCUS BM395985 31 bp mRNA linear EST 17-JAN-2002
 DEFINITION Tetrahymena thermophila cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

VERSION BM395985.1 GI:18196038

KEYWORDS

SOURCE

ORGANISM

Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE

1 (bases 1 to 31)
 /db_xref="taxon:5911"

AUTHORS

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.

TITLE

EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL

Unpublished (2002)

COMMENT

Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..31
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 32.3%; Score 10; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.6e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCGCCACCG 10
 |||||
 Db 24 TCGCCACCG 15

RESULT 6

BM397227/c
 LOCUS BM397227 18 bp mRNA linear EST 17-JAN-2002
 DEFINITION 5009-0-3-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION

VERSION BM397227.1 GI:18197280

KEYWORDS

SOURCE

ORGANISM

Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE

1 (bases 1 to 18)
 /db_xref="taxon:5911"

AUTHORS

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.

TITLE

EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL

Unpublished (2002)

COMMENT

Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..18
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CCGCCACCG 10
 |||||
 Db 17 CCGCCACCG 9

RESULT 7

BM400126/c

LOCUS BM400126 18 bp mRNA linear EST 17-JAN-2002

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM400126

VERSION BM400126.1 GI:18200179

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE

1 (bases 1 to 18)
 /db_xref="taxon:5911"

AUTHORS

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.

TITLE

EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL

Unpublished (2002)

COMMENT

Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..18
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCG 10
 |||
 Db 18 CCGCCACCG 10

RESULT 8

BM397047/c 19 bp mRNA linear EST 17-JAN-2002
 LOCUS BM397047
 DEFINITION 5009-0-28-D04.t.2 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397047

VERSION

BM397047.1 GI:18197100

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

ORGANISM

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
 1 (bases 1 to 19)
 Turkewitz.A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
 Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCG 10
 |||
 Db 19 CCGCCACCG 11

RESULT 9

BM397791/c 19 bp mRNA linear EST 17-JAN-2002
 LOCUS BM397791
 DEFINITION 5009-0-37-B02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397791

VERSION

BM397791.1 GI:18197844

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

ORGANISM

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE

AUTHORS

1 (bases 1 to 19)

TITLE

Turkewitz.A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

JOURNAL

Frankel,J. and Klobutcher,L.

COMMENT

EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCG 10
 |||
 Db 18 CCGCCACCG 10

RESULT 10

BM398839/c

LOCUS

BM398839

DEFINITION

5009-0-5-P03.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM398839

VERSION

BM398839.1 GI:18198892

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Turkewitz.A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

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 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Query Match 29.0%; Score 9; DB 3; Length 19;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION BM39882
VERSION BM39882.1 GI:18198935
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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sequence.
ACCESSION AJ685250
VERSION AJ685250.1 GI:49417840
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics

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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
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R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
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EH25 9PS, www.arkgenomics.org.
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5009-0-31-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397370
VERSION BM397370.1 GI:18197423
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 20)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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DEFINITION 5009-0-40-B03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398074
VERSION     BM398074.1 GI:18198127
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
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            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3

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RESULT 15
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LOCUS      20 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-45-F11.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398469
VERSION     BM398469.1 GI:18198522
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374,
            Fax: 773 702 3172
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 04:27:38 ; Search time 93 Seconds
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592.521 Million cell updates/sec

Title: US-10-688-489-59

Perfect score: 31

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Searched: 1303057 seqs, 888780828 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	11	35.5	19	6	PCT-US93-09232-14
C 5	11	35.5	22	3	US-09-811-838-20
C 6	11	35.5	24	2	US-08-229-781-14
C 7	11	35.5	24	2	US-08-630-918-14
C 8	11	35.5	24	3	US-09-004-422-14
C 9	11	35.5	24	3	US-09-918-568-14
C 10	11	35.5	24	3	US-10-126-120-3
C 11	11	35.5	25	3	US-08-118-200-5
C 12	11	35.5	25	3	US-08-458-745-5
C 13	11	35.5	25	3	US-09-876-176-5
C 14	11	35.5	25	3	US-09-396-196G-20729
C 15	11	35.5	25	3	US-09-396-196G-20730
C 16	11	35.5	25	3	US-09-396-196G-20731
C 17	11	35.5	25	3	US-09-396-196G-32281
C 18	11	35.5	25	3	US-09-396-196G-76882
C 19	11	35.5	25	3	US-09-396-196G-85134
C 20	11	35.5	25	3	US-09-396-196G-101638
C 21	11	35.5	25	3	US-09-396-196G-101639
C 22	11	35.5	25	3	US-09-396-196G-101640
C 23	11	35.5	31	3	US-10-126-120-19
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26	10	32.3	18	3	US-09-184-658-62	Sequence 62, Appl
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28	10	32.3	18	3	US-09-504-262D-62	Sequence 62, Appl
29	10	32.3	18	3	US-09-953-318-4	Sequence 4, Appl
30	10	32.3	18	3	US-09-477-962-46	Sequence 46, Appl
31	10	32.3	19	2	US-08-211-202-23	Sequence 23, Appl
32	10	32.3	19	2	US-08-244-597-21	Sequence 21, Appl
33	10	32.3	19	3	US-08-665-202-113	Sequence 113, Appl
34	10	32.3	19	3	US-09-315-574-113	Sequence 113, Appl
35	10	32.3	19	3	US-09-197-224-21	Sequence 21, Appl
c 36	10	32.3	19	3	US-09-422-978-4257	Sequence 4257, Ap
37	10	32.3	19	3	US-09-197-221-21	Sequence 21, Appl
38	10	32.3	19	3	US-09-572-392A-21	Sequence 21, Appl
39	10	32.3	19	3	US-09-723-756-21	Sequence 21, Appl
40	10	32.3	19	3	US-09-532-840-21	Sequence 21, Appl
41	10	32.3	20	2	US-08-031-143B-19	Sequence 19, Appl
c 42	10	32.3	20	2	US-08-167-113-19	Sequence 19, Appl
c 43	10	32.3	20	2	US-08-167-113-20	Sequence 20, Appl
c 44	10	32.3	20	2	US-08-313-185-22	Sequence 22, Appl
c 45	10	32.3	20	2	US-08-649-046-4	Sequence 4, Appl

ALIGNMENTS

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; Sequence 116529, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116529

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Qy 8 CCGGAAGTTGAG 19
Db 18 CCGGAAGTTGAG 7

RESULT 2
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; Sequence 116530, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

US-08-229-781-14/c
; Sequence 14, Application US/08229781
; Patent No. 5589174
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,781
; FILING DATE: April 19, 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
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; ORGANISM:
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; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
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; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
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; LOCATION:
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; Sequence 14, Application US/08630918
; Patent No. 5631350
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
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; SOFTWARE: Wordperfect 5.1
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; FILING DATE: April 5, 1996
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; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-630-918-14
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Best Local Similarity 100.0%; Pred. No. 5.5e+03;
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Db 12 AGTTGAGTAGA 2
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; Sequence 14, Application US/09004422
; Patent No. 6337070
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
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; APPLICATION NUMBER: US/09/004,422
; FILING DATE: January 8, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/443,862
; FILING DATE: May 22, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
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; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
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; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
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; OTHER INFORMATION:

; PUBLICATION INFORMATION:
; AUTHORS:
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; PUBLICATION DATE:
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Db 12 AGTTGAGTAGA 2
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|||
RESULT 9
US-09-918-568-14/c
; Sequence 14, Application US/09918568
; Patent No. 6720409
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/918,568
; FILING DATE: 02-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/004,422
; FILING DATE: January 8, 1998
; APPLICATION NUMBER: 08/443,862
; FILING DATE: May 22, 1995
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
; HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: <Unknown>
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-918-568-14
Query Match 35.5%; Score 11; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AGTTGAGTAGA 23
|||||

Db 12 AGTTGAGTAGA 2

RESULT 10
US-10-126-120-3/c
Sequence 3, Application US/10126120
Patent No. 6893825
GENERAL INFORMATION:
APPLICANT: Sakakibara, Hitoshi
TITLE OF INVENTION: Takel, Kentaro
FILE REFERENCE: 11127-004001
CURRENT APPLICATION NUMBER: US/10/126,120
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: JP 2001-291059
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC DNA

Query Match 35.5%; Score 11; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GGAAGTTGAGT 20
|||||

Db 21 GGAAGTTGAGT 11

RESULT 11
US-08-118-200-5
Sequence 5, Application US/08118200
Patent No. 6197500
GENERAL INFORMATION:
APPLICANT: SUTHERLAND, Grant R
APPLICANT: RICHARDS, Robert I
APPLICANT: SCHLESSINGER, David
APPLICANT: NAGARAJA, Ramaiah
APPLICANT: KREMER, Eric J
APPLICANT: YU, Sui
APPLICANT: BAKER, Elizabeth
APPLICANT: MULLEY, John C
APPLICANT: MANDEL, Jean-Louis
APPLICANT: PRITCHARD, Melanie April
APPLICANT: LYNCH, Michael
TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
FILING DATE: 09-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
FILING DATE: 20-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/638,518
FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,517
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 020160-164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-118-200-5

Query Match 35.5%; Score 11; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGA 18
|||||
Db 8 CCGGAAGTTGA 18

RESULT 12
US-08-458-745-5
; Sequence 5, Application US/08458745
; Patent No. 6242576
; GENERAL INFORMATION:
; APPLICANT: SUTHERLAND, Grant R
; APPLICANT: RICHARDS, Robert I
; APPLICANT: SCHLESSINGER, David
; APPLICANT: NAGARAJA, Ramiah
; APPLICANT: KREMER, Eric J
; APPLICANT: YU, Sui
; APPLICANT: BAKER, Elizabeth
; APPLICANT: MULLEY, John C
; APPLICANT: MANDEL, Jean-Louis
; APPLICANT: PRITCHARD, Melanie April
; APPLICANT: LYNCH, Michael
; TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
; TITLE OF INVENTION: FRAGILE X SYNDROME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,745
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/118,200
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: US 07/802,650
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,232
; FILING DATE: 20-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/638,518
; FILING DATE: 04-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,517
; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 020160-164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-458-745-5

Query Match 35.5%; Score 11; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGA 18
|||||
Db 8 CCGGAAGTTGA 18

RESULT 13
US-09-876-176-5/c
; Sequence 5, Application US/09876176
; Patent No. 6586244
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Den-Otter, Douglas R.
; APPLICANT: Winter, Jill A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: NEOPLASTIC DISEASE USING INHIBITORS OF LAMININ5BETA3
; FILE REFERENCE: PP-01702.002/200130.523
; CURRENT APPLICATION NUMBER: US/09/876.176
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Control oligonucleotide
US-09-876-176-5

Query Match 35.5%; Score 11; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGT 20
|||||
Db 20 GGAAGTTGAGT 10

RESULT 14
US-09-396-196G-20729
; Sequence 20729, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20729
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-20729

Query Match 35.5%; Score 11; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGACGGTGCTG 31
|||||
Db 10 AGACGGTGCTG 20

RESULT 15

US-09-396-196G-20730
 ; Sequence 20730, Application US/09396196G
 ; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20730

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-20730

Query Match 35.5%; Score 11; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGACGGTGCTG 31

Db 6 AGACGGTGCTG 16

Search completed: December 12, 2005, 05:41:02

Job time : 93 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 05:06:54 ; Search time 419 Seconds
(without alignments)
611.816 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcaccggaagttagtagacggtgctg 31

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9450414

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : Published Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	31	8	US-10-688-489-59
2	22	71.0	22	8	US-10-688-489-68
3	21	67.7	21	8	US-10-688-489-63
4	21	67.7	21	8	US-10-688-489-67
5	21	67.7	21	8	US-10-688-489-70
6	20	64.5	20	8	US-10-688-489-62
7	20	64.5	20	8	US-10-688-489-69
8	20	64.5	20	8	US-10-688-489-71
9	20	64.5	20	9	US-10-985-805-52
10	19	61.3	19	8	US-10-688-489-60
11	19	61.3	19	8	US-10-688-489-66
12	18	58.1	18	8	US-10-688-489-64
13	18	58.1	18	8	US-10-688-489-61
14	18	58.1	26	8	US-10-688-489-147
15	17	54.8	18	8	US-10-688-489-65
16	15	48.4	21	8	US-10-688-489-104
17	15	48.4	22	5	US-10-688-489-185
18	15	48.4	25	8	US-10-688-489-27587
19	15	48.4	28	8	US-10-688-489-186
20	14	45.2	25	10	US-11-036-317-721195
21	13	41.9	18	6	US-10-265-689-39
22	13	41.9	19	8	US-10-688-489-105
23	13	41.9	21	9	US-10-871-841-48

C 24	13	41.9	25	7	US-10-719-956-465218	Sequence 465218, A
C 25	13	41.9	25	8	US-10-719-900-67606	Sequence 67606, A
C 26	13	41.9	25	8	US-10-719-900-228204	Sequence 228204, A
C 27	13	41.9	25	8	US-10-719-900-380938	Sequence 380938, A
C 28	13	41.9	25	10	US-11-036-317-845552	Sequence 845552, A
C 29	12	38.7	18	8	US-10-688-489-178	Sequence 178, App
C 30	12	38.7	18	8	US-10-688-489-181	Sequence 181, App
C 31	12	38.7	21	10	US-11-110-517-1	Sequence 1, Appli
C 32	12	38.7	25	5	US-10-098-263B-48220	Sequence 48220, A
C 33	12	38.7	25	5	US-10-098-263B-55468	Sequence 55468, A
C 34	12	38.7	25	5	US-10-098-263B-84603	Sequence 84603, A
C 35	12	38.7	25	5	US-10-098-263B-84604	Sequence 84604, A
C 36	12	38.7	25	5	US-10-098-263B-101297	Sequence 101297, A
C 37	12	38.7	25	5	US-10-098-263B-130532	Sequence 130532, A
C 38	12	38.7	25	7	US-10-719-956-87744	Sequence 87744, A
C 39	12	38.7	25	7	US-10-719-956-109527	Sequence 109527, A
C 40	12	38.7	25	7	US-10-719-956-243826	Sequence 243826, A
C 41	12	38.7	25	7	US-10-719-956-447257	Sequence 447257, A
C 42	12	38.7	25	7	US-10-719-956-599493	Sequence 599493, A
C 43	12	38.7	25	7	US-10-719-956-623888	Sequence 623888, A
C 44	12	38.7	25	7	US-10-719-956-672084	Sequence 672084, A
C 45	12	38.7	25	8	US-10-719-900-21898	Sequence 21898, A

ALIGNMENTS

RESULT 1
US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication NO. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Jeffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 31
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-59

Query Match 100.0%; Score 31; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
Db 1 TCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2
US-10-688-489-68
; Sequence 68, Application US/10688489
; Publication NO. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 22
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-68
```

```
Query Match 71.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 GGAAGTTGAGTAGACGGTGCTG 31
    |||||
DB 1 CGAAGTTGAGTAGACGGTGCTG 22
```

RESULT 3

```
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Jeffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-63
```

```
Query Match 67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCCGCCACCGGAAGTTGAGTA 21
    |||||
DB 1 TCCGCCACCGGAAGTTGAGTA 21
```

RESULT 4

```
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-67
```

```
Query Match 67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 10 GGAAGTTGAGTAGACGGTGCT 30
    |||||
DB 1 CGAAGTTGAGTAGACGGTGCT 21
```

RESULT 5

```
US-10-688-489-70
; Sequence 70, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 21
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-70
```

```
Query Match 67.7%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 11 GAAGTTGAGTAGACGGTGCTG 31
    |||||
DB 1 GAAGTTGAGTAGACGGTGCTG 21
```

RESULT 6

```
US-10-688-489-62
```


; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGAAGTTGAGT 20
|||||
Db 1 TCCGCCACCGAAGTTGAGT 20

RESULT 7

US-10-688-489-69
; Sequence 69, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-69

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GAAGTTGAGTAGACGGTGCT 30
|||||
Db 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 8

US-10-688-489-71
; Sequence 71, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-71

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGACGGTGCTG 31
|||||
Db 1 AAGTTGAGTAGACGGTGCTG 20

RESULT 9

US-10-985-805-52
; Sequence 52, Application US/10985805
; Publication No. US20050130133A1
; GENERAL INFORMATION:
; APPLICANT: Burde, Stefan H.M.
; APPLICANT: Gierman, Todd M.
; APPLICANT: Glenn, Christopher C.
; TITLE OF INVENTION: Oligonucleotides and Methods for Detection of West Nile Virus
; FILE REFERENCE: 7430*201
; CURRENT APPLICATION NUMBER: US/10/985,805
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/519,096
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-985-805-52

Query Match 64.5%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGAGTAGA 23
|||||
Db 1 GCCACCGGAAGTTGAGTAGA 20

RESULT 10

US-10-688-489-60
; Sequence 60, Application US/10688489

Publication No. US20040259108A1
GENERAL INFORMATION:
Sequence 66, Application US/10688489
Publication No. US20040259108A1
APPLICANT: Linnen, Jeffrey M.
APPLICANT: Pollner, Reinhold B.
APPLICANT: Wu, Wen
APPLICANT: Dennis, Geoffrey G.
APPLICANT: Darby, Paul M.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GPI40-04.UT
CURRENT APPLICATION NUMBER: US/10/688,489
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/418,891
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/429,006
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/449,810
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 19
TYPE: DNA
ORGANISM: West Nile Virus
US-10-688-489-60

Query Match 61.3%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCCACCGGAAGTTGAG 19
|||||
DB 1 TCCGCCACCGGAAGTTGAG 19

RESULT 11
US-10-688-489-66
Sequence 66, Application US/10688489
Publication No. US20040259108A1
GENERAL INFORMATION:
APPLICANT: Linnen, Jeffrey M.
APPLICANT: Pollner, Reinhold B.
APPLICANT: Wu, Wen
APPLICANT: Dennis, Geoffrey G.
APPLICANT: Darby, Paul M.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GPI40-04.UT
CURRENT APPLICATION NUMBER: US/10/688,489
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/418,891
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/429,006
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/449,810
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 66
LENGTH: 19
TYPE: DNA
ORGANISM: West Nile Virus
US-10-688-489-66

Query Match 61.3%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGAGTA 21
|||||
DB 1 CGCCACCGGAAGTTGAGTA 19

RESULT 12
US-10-688-489-64
Sequence 64, Application US/10688489
Publication No. US20040259108A1
GENERAL INFORMATION:
APPLICANT: Linnen, Jeffrey M.
APPLICANT: Pollner, Reinhold B.
APPLICANT: Wu, Wen
APPLICANT: Dennis, Geoffrey G.
APPLICANT: Darby, Paul M.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GPI40-04.UT
CURRENT APPLICATION NUMBER: US/10/688,489
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/418,891
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/429,006
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/449,810
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 64
LENGTH: 18
TYPE: DNA
ORGANISM: West Nile Virus
US-10-688-489-64

Query Match 58.1%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCACCGGAAGTTGAGT 20
|||||
DB 1 CGCCACCGGAAGTTGAGT 18

RESULT 13
US-10-688-489-61
Sequence 61, Application US/10688489
Publication No. US20040259108A1
GENERAL INFORMATION:
APPLICANT: Linnen, Jeffrey M.
APPLICANT: Pollner, Reinhold B.
APPLICANT: Wu, Wen
APPLICANT: Dennis, Geoffrey G.
APPLICANT: Darby, Paul M.
TITLE OF INVENTION: Compositions and Methods for Detecting
FILE REFERENCE: GPI40-04.UT
CURRENT APPLICATION NUMBER: US/10/688,489
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/418,891
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/429,006
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/449,810
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 196
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 19
TYPE: DNA
ORGANISM: West Nile Virus
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)...(1)
OTHER INFORMATION: I
US-10-688-489-61

Query Match 58.1%; Score 18; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGCCACCGAAGTTGAG 19
Db 2 CCGCCACCGAAGTTGAG 19

RESULT 14

US-10-688-489-147/c
; Sequence 147, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE OF INVENTION: West Nile Virus
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 147
; LENGTH: 26
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(26)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-147

Query Match 58.1%; Score 18; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTGAGTAGACGGTGCTG 31
Db 26 GTTGAGTAGACGGTGCTG 9

RESULT 15

US-10-688-489-65
; Sequence 65, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE OF INVENTION: West Nile Virus
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65

; LENGTH: 18
; TYPE: DNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(1)
; OTHER INFORMATION: I
US-10-688-489-65

Query Match 54.8%; Score 17; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAAGTTGACT 20
Db 2 GCCACCGGAAGTTGACT 18

Search completed: December 12, 2005, 06:38:57
Job time : 419 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 05:39:28 ; Search time 119 Seconds
(without alignments)
97.391 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tcgcaccggaagttagtagcgtgctg 31

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 3392430 seqs, 186927314 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6558440

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : Published Applications_NA_New.*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	41.9	19	8	US-11-101-244-893396
2	13	41.9	19	8	US-11-101-244-1142294
3	13	41.9	19	8	US-11-101-244-1142294
4	13	41.9	19	9	US-11-101-244-1558548
5	13	41.9	19	9	US-11-101-244-893396
6	13	41.9	19	9	US-11-101-244-1142294
7	12	38.7	19	8	US-11-101-244-1558548
8	12	38.7	19	8	US-11-101-244-203873
9	12	38.7	19	8	US-11-101-244-203933
10	12	38.7	19	8	US-11-101-244-252961
11	12	38.7	19	8	US-11-101-244-289277
12	12	38.7	19	8	US-11-101-244-301698
13	12	38.7	19	8	US-11-101-244-730807
14	12	38.7	19	8	US-11-101-244-734540
15	12	38.7	19	8	US-11-101-244-769352
16	12	38.7	19	8	US-11-101-244-769426
17	12	38.7	19	8	US-11-101-244-941002
18	12	38.7	19	8	US-11-101-244-941012
19	12	38.7	19	8	US-11-101-244-1104174
20	12	38.7	19	8	US-11-101-244-1104183
21	12	38.7	19	8	US-11-101-244-1339290
22	12	38.7	19	8	US-11-101-244-1360771
23	12	38.7	19	8	US-11-101-244-1370517
					Sequence 1513933,

c 24	12	38.7	19	8	US-11-101-244-1550584	Sequence 1550584,
c 25	12	38.7	19	8	US-11-101-244-1550586	Sequence 1550586,
c 26	12	38.7	19	8	US-11-101-244-1550608	Sequence 1550608,
c 27	12	38.7	19	9	US-11-083-784-203873	Sequence 203873,
c 28	12	38.7	19	9	US-11-083-784-203933	Sequence 203933,
c 29	12	38.7	19	9	US-11-083-784-252961	Sequence 252961,
c 30	12	38.7	19	9	US-11-083-784-289277	Sequence 289277,
c 31	12	38.7	19	9	US-11-083-784-301698	Sequence 301698,
c 32	12	38.7	19	9	US-11-083-784-730807	Sequence 730807,
c 33	12	38.7	19	9	US-11-083-784-734540	Sequence 734540,
c 34	12	38.7	19	9	US-11-083-784-769352	Sequence 769352,
c 35	12	38.7	19	9	US-11-083-784-769426	Sequence 769426,
c 36	12	38.7	19	9	US-11-083-784-941002	Sequence 941002,
c 37	12	38.7	19	9	US-11-083-784-941012	Sequence 941012,
c 38	12	38.7	19	9	US-11-083-784-1104174	Sequence 1104174,
c 39	12	38.7	19	9	US-11-083-784-1104183	Sequence 1104183,
c 40	12	38.7	19	9	US-11-083-784-1339290	Sequence 1339290,
c 41	12	38.7	19	9	US-11-083-784-1360771	Sequence 1360771,
c 42	12	38.7	19	9	US-11-083-784-1370517	Sequence 1370517,
c 43	12	38.7	19	9	US-11-083-784-1513933	Sequence 1513933,
c 44	12	38.7	19	9	US-11-083-784-1550584	Sequence 1550584,
c 45	12	38.7	19	9	US-11-083-784-1550586	Sequence 1550586,

ALIGNMENTS

RESULT 1
US-11-101-244-893396
; Sequence 893396, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 893396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-893396

Query Match 41.9%; Score 13; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 98;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGGAAGTTGAG 19
|||||:|:
DB 2 ACCGGAAGTUGAG 14

RESULT 2
US-11-101-244-1142294/c
; Sequence 1142294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1142294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1142294

Query Match      41.9%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GTAGACGGTGCTG 31
Db 16 GTAGACGGTGCTG 4

RESULT 3
US-11-101-244-1558548/c
; Sequence 1558548, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1558548
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1558548

Query Match      41.9%; Score 13; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAG 22
Db 13 GGAAGTTGAGTAG 1

RESULT 4
US-11-083-784-893396
; Sequence 893396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 893396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-893396

Query Match      41.9%; Score 13; DB 9; Length 19;
Best Local Similarity 84.6%; Pred. No. 98;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGGAAGTTGAG 19
Db 2 ACCGGAAGUUGAG 14

RESULT 5
US-11-083-784-1142294/c
; Sequence 1142294, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1142294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1142294

Query Match      41.9%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GTAGACGGTGCTG 31
Db 16 GTAGACGGTGCTG 4

RESULT 6
US-11-083-784-1558548/c
; Sequence 1558548, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1558548
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1558548

Query Match 41.9%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGAAGTTGAGTAG 22
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Db 13 GGAAGTTGAGTAG 1

RESULT 7

US-11-101-244-203873/c
; Sequence 203873, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 203873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-203873

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGAG 19
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Db 15 CCGGAAGTTGAG 4

RESULT 8

US-11-101-244-203933/c
; Sequence 203933, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; SEQ ID NO 203933
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-203933

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGGAAGTTGAG 19
|||||
Db 15 CCGGAAGTTGAG 4

RESULT 9

US-11-101-244-252961/c
; Sequence 252961, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 252961
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-252961

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TGAGTAGACGGT 27
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Db 17 TGAGTAGACGGT 6

RESULT 10

US-11-101-244-289277
; Sequence 289277, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 289277
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-289277

Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGGAGCTTGAGT 20
Db 4 CGGAGGUGAGU 15
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RESULT 11
US-11-101-244-301698
; Sequence 301698, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 301698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-301698

Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGGAGTT 16
Db 8 CCACCGGAGU 19
|||||:||||:

RESULT 12
US-11-101-244-730807
; Sequence 730807, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 730807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-730807

Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 91.7%; Pred. No. 3.6e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACCGGAGCT 15
Db 8 GCCACCGGAGU 19
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RESULT 13
US-11-101-244-734540
; Sequence 734540, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 734540
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-734540

Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAGTTGAGTAGA 23
Db 2 AAGUUGAGUAGA 13
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RESULT 14
US-11-101-244-769352/c
; Sequence 769352, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-769352

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Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      10  GGAAGTTGAGTA 21
Db      13  GGAAGTTGAGTA 2

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RESULT 15
US-11-101-244-769426/c
; Sequence 769426, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 769426
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-769426

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Query Match      38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      10  GGAAGTTGAGTA 21
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 24
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Searched: 5883141 seqs, 2842172563 residues

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Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

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SUMMARIES

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2	11	45.8	22	BD103599
3	11	45.8	22	AX021007 Sequence
C 4	11	45.8	23	AR487560 Sequence
5	10	41.7	22	A64826 Sequence 2
6	10	41.7	22	BD182575 Gene tran
C 7	10	41.7	22	CS110845 Sequence
C 8	10	41.7	22	CS111631 Sequence
C 9	10	41.7	22	AR219168 Sequence
C 10	10	41.7	22	AX657380 Sequence
C 11	10	41.7	23	AR090696 Sequence
C 12	10	41.7	23	AR091566 Sequence
C 13	10	41.7	23	AR154050 Sequence
C 14	10	41.7	23	BD130156 Material
C 15	10	41.7	23	BD134794 Method an
C 16	10	41.7	23	CQ890765 Sequence
17	10	41.7	23	CQ897305 Sequence
18	10	41.7	23	CQ898454 Sequence

C 19	10	41.7	23	6	CQ967582 Sequence
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C 21	10	41.7	23	6	AR221816 Sequence
C 22	10	41.7	23	6	AR225985 Sequence
C 23	10	41.7	23	6	AR565274 Sequence
C 24	10	41.7	23	6	AR584243 Sequence
25	10	41.7	24	6	A57695 Sequence 5
26	10	41.7	24	6	A76942 Sequence 4
C 27	10	41.7	24	6	AR084744 Sequence
28	10	41.7	24	6	CS083207 Sequence
29	10	41.7	24	6	AR239100 Sequence
C 30	10	41.7	24	6	AR360527 Sequence
C 31	10	41.7	24	6	AR563493 Sequence
C 32	10	41.7	24	6	AR581468 Sequence
C 33	10	41.7	24	6	AX055394 Sequence
34	10	41.7	24	6	AX077055 Sequence
35	10	41.7	24	6	AX080779 Sequence
C 36	10	41.7	24	6	AX278902 Sequence
C 37	10	41.7	24	6	AX289492 Sequence
C 38	10	41.7	24	6	AX291060 Sequence
C 39	10	41.7	24	6	AX291739 Sequence
40	10	41.7	24	6	AX447095 Sequence
C 41	10	41.7	24	6	AX795373 Sequence
42	9	37.5	22	6	AR017548 Sequence
C 43	9	37.5	22	6	AR117174 Sequence
C 44	9	37.5	22	6	AR119281 Sequence
C 45	9	37.5	22	6	AR136780 Sequence

ALIGNMENTS

RESULT 1
AR568140/c
LOCUS AR568140 22 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 65 from patent US 6781028.
ACCESSION AR568140
VERSION AR568140.1 GI:53986427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Costa,M.R., Doberstein,S.K., Elson,S.L., Ferguson,K.C. and Homburger,S.A.
TITLE Animal models and methods for analysis of lipid metabolism and screening of pharmaceutical and pesticidal agents that modulate lipid metabolism
JOURNAL Patent: US 6781028-A 65 24-AUG-2004;
FEATURES Exellxis, Inc.; South San Francisco, CA
source location/Qualifiers
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Query Match 50.0%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 GTTCTGAGGCT 21
Db 15 GTTCTGAGGCT 4

RESULT 2
BD103599 22 bp DNA linear PAT 27-AUG-2002
LOCUS BD103599
DEFINITION Mood disorder gene.
ACCESSION BD103599
VERSION BD103599.1 GI:22649173
KEYWORDS JP 2001526897-A/13.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Broekhoven,C.V., Raeymaekers,P. and Favero,J.D.
TITLE Mood disorder gene
JOURNAL VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE
COMMENT OS Homo sapiens (human)
PN JP 2001526897-A/13
PD 25-DEC-2001
PF 17-DEC-1998 JP 2000525561
PR 18-DEC-1997 GB 9726804.9
PI CHRISTINE VAN BROECKHOVEN,PETER RAEYMAEKERS,JURGEN DEL FAVERO
PC C12N15/09,A01K67/027,A61K38/00,A61P25/22,A61P25/24,C07K14/47,
PC C12N5/10,
PC C12Q1/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/00 CC Mood
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 6 ACGGTTCTGAG 16
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AX021007
LOCUS AX021007 22 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from Patent WO9932643.
ACCESSION AX021007
VERSION AX021007.1 GI:10044670
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.
TITLE Mood disorder gene
JOURNAL Patent: WO 9932643-A 13 01-JUL-1999;
BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 ACGGTTCTGAG 17
|||||
Db 6 ACGGTTCTGAG 16
RESULT 4
AX021007
LOCUS AX021007 22 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from Patent WO9932643.
ACCESSION AX021007
VERSION AX021007.1 GI:10044670
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.
TITLE Mood disorder gene
JOURNAL Patent: WO 9932643-A 13 01-JUL-1999;
BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
FEATURES source
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 ACGGTTCTGAG 17
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Db 6 ACGGTTCTGAG 16
RESULT 5
A64826
LOCUS A64826 22 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 2 from Patent WO9730178.
ACCESSION A64826
VERSION A64826.1 GI:4530817
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Neri,C., Cann,H.M. and Cohen,D.
TITLE DIAGNOSING TRINUCLEOTIDE REPEAT DISEASES AND GENES INVOLVED THEREIN
JOURNAL Patent: WO 9730178-A 2 21-AUG-1997;
FONDATION JEAN DAUSSET CEPH (FR)
COMMENT Other publication PR 2745007 19970822.
FEATURES source
Location/Qualifiers
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GENETICS"
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Query Match 41.7%; Score 10; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 CTGAGGGCTT 22
|||||
Db 4 CTGAGGGCTT 13
RESULT 6
BD182575
LOCUS BD182575 22 bp DNA linear PAT 15-MAY-2003
DEFINITION Gene transfer of angiogenesis factor into dermatosis.
ACCESSION BD182575
VERSION BD182575.1 GI:30793540
KEYWORDS WO 02089854-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
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other sequences; artificial sequences.
1 (bases 1 to 22)
Morishita,R., Nakanishi,K., Kaneda,Y. and Kotani,H.
Gene transfer of angiogenesis factor into dermatosis
Patent: WO 02089854-A 10 14-NOV-2002;
JOURNAL
ANGES MG INC,RYUICHI MORISHITA,KUNIAKI NAKANISHI,YASUFUMI KANEDA,
HITOSHI KOTANI
OS Artificial Sequence
PN WO 02089854-A/10
PD 14-NOV-2002
PF 09-MAY-2002 WO 2002JP004529
PR 09-MAY-2001 JP OIP 139373
PI RYUICHI MORISHITA,KUNIAKI NAKANISHI,YASUFUMI KANEDA,HITOSHI
KOTANI
PC A61K48/00,A61K38/22,A61P17/02,A61P17/14
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC key Location/Qualifiers
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FT source
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21
Db |||||||

RESULT 7
CS110845/c
LOCUS 22 bp DNA linear PAT 22-JUN-2005
DEFINITION Sequence 88 from Patent WO2005052161.
ACCESSION CS110845
VERSION CS110845.1 GI:68148949
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Jones,B.E., Kolkman,M., Leeflang,C., Poulouse,A.J., van der
Kleij,W.A. and van Marrewijk,L.(.
TITLE Serine proteases, nucleic acids encoding serine enzymes and vectors
and host cells incorporating same
JOURNAL Patent: WO 2005052161-A 88 09-JUN-2005;
Genencor International, Inc. (US)
FEATURES
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1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
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Query Match 41.7%; Score 10; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCGAGACGGT 11
Db |||||||

RESULT 8
AX657380/c
LOCUS 22 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 93 from Patent WO02100896.
ACCESSION AX657380
VERSION AX657380.1 GI:29160120
KEYWORDS

```

3

FT source 1..23
FT Location/Qualifiers
1..23
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 41.7%; Score 10; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CTGAGGGCTT 22
| | | | | | | |
Db 11 CTGAGGGCTT 20

RESULT 15
BD134794/c
LOCUS 23 bp DNA linear PAT 18-SEP-2002
DEFINITION Method and means of constructing safe and high-titer recombinant lentivirus vector.
ACCESSION BD134794
VERSION BD134794.1 GI:23229739
KEYWORDS JP 2002508184-A/19.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Nardini,L., Dall,T., Ferson,D.A. and Wit,R.
TITLE Method and means of constructing safe and high-titer recombinant lentivirus vector
JOURNAL Patent: JP 2002508184-A 19 19-MAR-2002;
CELL GENESYS INC

OS Unidentified
PN JP 2002508184-A/19
PD 19-MAR-2002
PF 11-DEC-1998 JP 2000539150
PR 12-DEC-1997 US 08/989394
PI LUIGI NARDINI, THOMAS DALL, DEBORAH A FERSON, ROCHEL WIT PC
CI 2002508184-A/19
CC Strandedness: Single;
CC Topology: Linear;
CC Method and means of constructing safe and high-titer CC recombinant
CC lentivirus vector
FH Key Location/Qualifiers
FT source 1..23
FT Location/Qualifiers
1..23
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source
ORIGIN
Query Match 41.7%; Score 10; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTGAGGGCT 21
| | | | | | | |
Db 21 TCTGAGGGCT 12

Search completed: December 12, 2005, 02:56:11
Job time : 1696 secs

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1	24	100.0	24	12	ADN36752	Adn36752	West Nile
2	24	100.0	24	12	ADN36753	Adn36753	West Nile
3	23	95.8	23	12	ADN36754	Adn36754	West Nile
4	22	91.7	22	12	ADN36755	Adn36755	West Nile
5	21	87.5	23	12	ADN36827	Adn36827	West Nile
6	11	45.8	22	2	AX89557	Aax89557	Human chr
7	11	45.8	22	6	ABQ74548	Abq74548	Human tra
8	11	45.8	22	12	ADL90000	Adl90000	Gluconoba
9	11	45.8	22	13	ADS84984	Ads84984	Human lun
10	11	45.8	23	12	ADJ95450	Adj95450	Human ubi
11	11	45.8	23	13	ADS86872	Ads86872	Primer #2
12	11	45.8	23	14	ADZ75830	Adz75830	Human E3a
13	11	45.8	24	8	RAL51429	Ral51429	Human cys
14	10	41.7	22	2	AT85654	Atc85654	Primer Co
15	10	41.7	22	2	AX09818	Aax09818	Human bia
16	10	41.7	22	2	AX28696	Aax28696	Nucleotid
17	10	41.7	22	4	AAF29770	Aaf29770	Pucrenili
18	10	41.7	22	5	AAF24279	Aaf24279	Snrpn tra
19	10	41.7	22	5	AA523206	Aas23206	Human COL

CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitoes, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.

XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGCTTAC 24
Db 1 TCCGAGACGGTCTCTGAGGCTTAC 24

RESULT 2

ADN36753
ID ADN36753 standard; DNA; 24 BP.

XX AC ADN36753;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID75.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 26; SEQ ID NO 75; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.

SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGCTTAC 24
Db 1 TCCGAGACGGTCTCTGAGGCTTAC 24

RESULT 3

ADN36754
ID ADN36754 standard; DNA; 23 BP.

XX AC ADN36754;

XX DT 15-JUL-2004 (first entry)

XX DE West Nile virus detection-related oligonucleotide probe SeqID76.

XX KW hybridisation assay probe; nucleic acid detection;

XX KW target-complementary sequence; flavivirus; West Nile virus; WNV;

XX KW RNA virus; infection; meningitis; encephalitis;

XX KW high throughput screening; probe; ss.

XX OS West Nile virus.

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX PT New hybridization assay probe comprising target-complementary sequence of
XX bases, useful in detecting flavivirus, e.g. West Nile virus.

XX PS Claim 26; SEQ ID NO 76; 135pp; English.

XX CC This invention relates to a novel hybridisation assay probe, for
XX detecting a nucleic acid, which is a probe sequence that comprises a
XX target-complementary sequence of bases, and optionally one or more base
XX sequences that are not complementary to the nucleic acid that is to be
XX detected. The hybridisation assay probes and the kits are useful in
XX detecting and amplifying a target nucleic acid sequence, for example
XX flavivirus like West Nile virus, that may be present in a biological
XX sample. West Nile virus (WNV) is an RNA virus that primarily infects
XX birds and culex mosquitoes, with humans and horses serving as incidental
XX hosts. Infection of humans can lead to meningitis or encephalitis. The
XX invention may allow for accurate and efficient high throughput screening.
XX The present sequence is that of an oligonucleotide probe which is related
XX to the invention.

SQ Sequence 23 BP; 4 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 95.8%; Score 23; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTCTGAGGCTTA 23
Db 1 TCCGAGACGGTCTCTGAGGCTTA 23

```

RESULT 4
ADN36755
ID   ADN36755 standard; DNA; 22 BP.
XX
AC   ADN36755;
XX
DT   15-JUL-2004 (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID77.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
XX
PR   25-NOV-2002; 2002US-0429006P.
XX
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 77; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitoes, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;
      Query Match      91.7%; Score 22; DB 12; Length 22;
      Best Local Similarity 100.0%; Pred. No. 0.011;
      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TCCGAGACGGTTCGAGGCTT 22
      |||||
Db   1 TCCGAGACGGTTCGAGGCTT 22
      |||||

RESULT 5
ADN36827
ID   ADN36827 standard; RNA; 23 BP.
XX
AC   ADN36827;
XX
DT   15-JUL-2004 (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID149.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
XX
PR   25-NOV-2002; 2002US-0429006P.
XX
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 77; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitoes, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;
      Query Match      91.7%; Score 22; DB 12; Length 22;
      Best Local Similarity 100.0%; Pred. No. 0.011;
      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TCCGAGACGGTTCGAGGCTT 22
      |||||
Db   1 TCCGAGACGGTTCGAGGCTT 22
      |||||

```

```

XX   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
XX
PR   25-NOV-2002; 2002US-0429006P.
XX
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Example 1; SEQ ID NO 149; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitoes, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 23 BP; 5 A; 4 C; 8 G; 0 T; 6 U; 0 Other;
      Query Match      87.5%; Score 21; DB 12; Length 23;
      Best Local Similarity 76.2%; Pred. No. 0.038;
      Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY   4 GAGACGGTTCGAGGCTTAC 24
      |||||
Db   1 GAGACGGUUCUGAGGGCUUAC 21
      |||||

RESULT 6
AAx88557
ID   AAx88557 standard; DNA; 22 BP.
XX
AC   AAx88557;
XX
DT   10-SEP-1999 (first entry)
XX
DE   Human chromosome 18q YAC clone amplification primer.
XX
KW   Human chromosome 18q; mood disorder; polymorphic marker; detection;
KW   identification; trinucleotide repeat expansion; schizophrenia;
KW   anxiety disorder; adjustment disorder; personality disorder;

```

```
KW nucleotide triplet repeat; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9932643-A2.
XX
XX 01-JUL-1999.
XX
XX 17-DEC-1998; 98WO-EP008543.
XX
XX 18-DEC-1997; 97GB-00026804.
XX
XX (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Van Broeckhoven C, Raeymaekers P, Del-Favero J;
XX
XX WPI; 1999-418934/35.
XX
XX Detecting nucleotide triplet repeats in human chromosome 18q.
XX
XX Claim 29; Fig 15b; 87pp; English.
XX
XX The present invention describes detecting nucleotide triplet repeats in a
XX region of human chromosome 18q disposed between polymorphic markers
XX D18S68 and D18S979 to identify a human gene associated with a mood
XX disorder or related disorder. AAX88542 to AAX88705 represents human
XX chromosome 18q YAC clones and primers corresponding to them used in the
XX exemplification of the present invention. YAC clones comprising a portion
XX of the region of human chromosome 18q between markers D18S68 and D18S979
XX are used to identify at least one human gene associated with a mood
XX disorder or related disorder. The mood disorder or related disorder, is
XX chosen from the Diagnostic and Statistical Manual of Mental Disorders.
XX version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4,
XX 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1,
XX 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3),
XX adjustment disorders (309.XX) and personality disorders (codes 301.XX).
XX Probes derived from genes associated with the mood disorder or related
XX disorder can be used to detect pathological mutations or genetic
XX variations in patients. The methods, probes and antibodies can be used to
XX determine the susceptibility of an individual to a mood disorder or
XX related disorder. The nucleic acids and proteins of the human gene can be
XX used to treat mood disorders and related disorders
XX
XX Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 45.8%; Score 11; DB 2; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+04;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 ACGGTTCTGAG 17
XX Db 6 ACGGTTCTGAG 16
XX
XX RESULT 7
XX ABQ74548
XX ID ABQ74548 standard; DNA; 22 BP.
XX
XX AC ABQ74548;
XX
XX 22-OCT-2002 (first entry)
XX
XX Human transglutaminase-B PCR primer SEQ ID NO:16.
XX
XX Human; transglutaminase; transglutaminase-A; transglutaminase-B; TGWA;
XX TGMB; enzyme; Huntington's disease; neuroprotective; gene therapy;
XX Factor XIII antagonist; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200259265-A2.
XX
XX
```

```
PD 01-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-US050405.
XX
XX 21-DEC-2000; 2000US-0257754P.
XX
XX (DECO-) DECODE GENETICS INC.
XX
XX Gurney M, Hannesson HH;
XX
XX WPI; 2002-608452/65.
XX
XX New isolated nucleic acids of transglutaminase (TGM) A and TGM-B residing
XX on chromosome 15 and 20, respectively, useful for treating Huntington's
XX disease.
XX
XX Example 2; Page 49; 98pp; English.
XX
XX The present invention describes a human transglutaminase-A (TGMA) which
XX is located to chromosome 15 (more specifically 15q15), and a human
XX transglutaminase-B (TGM-B) which is located to chromosome 20. TGMA and
XX TGM-B have neuroprotective activity and can be used as Factor XIII
XX antagonist and in gene therapy. Nucleotide sequences encoding TGMA and
XX TGM-B can be used as molecular weight markers on Southern gels, and as
XX chromosome markers which are labeled to map related gene positions. They
XX can be used for deriving primers for genetic fingerprinting, for raising
XX anti-polypeptide antibodies using DNA immunisation techniques or as
XX antigen for raising anti-DNA antibodies or for eliciting immune
XX responses. Additionally, the nucleotide sequences are useful for
XX generating TGMs for identifying agents which alter the activity or
XX expression of TGMs, for identifying and expressing recombinant
XX polypeptides for analysis, characterisation or therapeutic use, and as
XX markers for tissues in which the corresponding polypeptide is expressed.
XX A TGM therapeutic agent is useful for treating Huntington's disease. The
XX present sequence represents a PCR primer for human TGM-B, which is used in
XX an example from the present invention
XX
XX Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 45.8%; Score 11; DB 6; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+04;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 14 TGAGGGCTTAC 24
XX Db 4 TGAGGGCTTAC 14
XX
XX RESULT 8
XX ADL90000
XX ID ADL90000 standard; DNA; 22 BP.
XX
XX AC ADL90000;
XX
XX 20-MAY-2004 (first entry)
XX
XX Gluconobacter oxydans NADH production-related NRF1 gene PCR primer #7.
XX
XX transaldolase activity; glucose-6-phosphate isomerase; NADH production;
XX target substance manufacture; NRF1; PCR; primer; ss.
XX
XX Gluconobacter oxydans.
XX
XX JP2004024140-A.
XX
XX 29-JAN-2004.
XX
XX 26-JUN-2002; 2002JP-00186487.
XX
XX 26-JUN-2002; 2002JP-00186487.
XX
XX (AJIN ) AJINOMOTO KK.
XX
```

CC	The present invention relates to a method for detecting the presence of a cancer cell in a patient. The method comprises: contacting a biological sample obtained from a patient with two or more PCR primers for a lung cancer-specific protein polynucleotide; amplifying the polynucleotides; and detecting the amplified polynucleotides, where the presence of the amplified polynucleotides indicates the presence of lung cancer cells in the patient. The method is useful in detecting the presence of a cancer cell, preferably lung cancer cell in a patient. The present sequence is a probe for one such lung cancer-specific gene protein used in the method of the invention.									
XX										
QQ	Sequence	22 BP; 5 A; 11 C; 5 G; 1 T; 0 U; 0 Other;								
CC	Query Match	45.8%;	Score	11;	DB	13;	Length	22;		
CC	Best Local Similarity	100.0%;	Pred. No.	1.6e+04;						
CC	Matches	11;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	9	GGTTCCTGAGGG	19							
Db	22	GGTTCCTGAGGG	12							
RESULT 10										
ADJ95450/c										
ID	ADJ95450 standard; DNA; 23 BP.									
XX	AC	ADJ95450;								
XX	AC	ADJ95450;								
DT	03-JUN-2004 (first entry)									
XX	Human Ubiquitin ligase E3alpha I PCR primer #4.									
DE										
XX	Human; ss; PCR; ubiquitin ligase; E3alpha I;									
KW	ubiquitin-proteasome pathway; gene therapy; vaccine; muscular atrophy;									
KW	cachexia; catabolic disorders; cancer cachexia; renal cachexia;									
KW	inflammatory cachexia; muscle wasting disorder; metabolic acidosis;									
KW	uremia; burn; hyperthyroidism; Cushing's syndrome; fasting;									
KW	denervation atrophy; diabetes mellitus; sepsis; AIDS wasting syndrome;									
KW	primer.									
XX										
OS	Homo sapiens.									
XX										
XX	US6706505-B1.									
XX										
PD	16-MAR-2004.									
XX										
PF	28-NOV-2000; 2000US-00724126.									
XX										
PR	08-MAR-2000; 2000US-0187911P.									
XX										
PA	(AMGE-) AMGEN INC.									
XX										
PI	Han H, Kwak K;									
XX										
DR	WPI; 2004-236723/22..									
XX										
PT	New nucleic acid molecule, useful for preparing a composition for									
PT	diagnosing, treating or preventing diseases associated with human									
PT	E3approximately polypeptide, e.g., muscle atrophy.									
XX										
XX										
PS	Example 1; SEQ ID NO 10; 104pp; English.									
XX										
CC	The invention relates to a new isolated nucleic acid molecule appearing									
CC	as ADJ95441 (or its complement) encoding a ubiquitin ligase E3alpha I									
CC	protein appearing as ADJ95442. Also included are a vector comprising the									
CC	nucleic acid, a host cell comprising the vector, a process of producing the									
CC	E3alpha I ubiquitin ligase polypeptide, a composition comprising the									
CC	nucleic acid molecule, a reagent comprising a detectably labelled									
CC	nucleotide, and a method for determining the presence of a human E3alpha									
CC	I ubiquitin ligase nucleic acid in a biological sample. The nucleic acid									
CC	molecule is useful for preparing a composition for diagnosing, treating									
CC	or preventing diseases associated with human E3alpha I polypeptide, e.g.									
CC	muscle atrophy, cachexia, catabolic disorders, cancer, cachexia, renal									

CC cachexia, inflammatory cachexia, muscle wasting disorders associated with
 CC metabolic acidosis, uremia, burns, hyperthyroidism, Cushing's syndrome,
 CC fasting, denervation atrophy, diabetes mellitus, sepsis and AIDS wasting
 CC syndrome. The present sequence is a PCR primer used to isolate cDNA
 CC encoding human E3alpha I.

XX Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 45.8%; Score 11; DB 12; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TTCTGAGGGCT 21
 |||||
 Db 23 TTCTGAGGGCT 13

RESULT 11
 ADS86872/c
 ID ADS86872 standard; DNA; 23 BP.
 XX
 AC ADS86872;
 DT 16-DEC-2004 (first entry)
 XX
 DE Primer #2294-37 for PCR of human E3alphaI ubiquitin ligase gene.
 XX
 KW Human; E3alpha ubiquitin ligase; huE3alphaI;
 KW ubiquitin-proteasome pathway; chromosome 15 q; rapid muscle wasting;
 KW fasting; metabolic acidosis; muscle degeneration; kidney failure;
 KW renal cachexia; uremia; diabetes mellitus; sepsis; AIDS wasting syndrome;
 KW cancer cachexia; negative nitrogen balance; burn; Cushing's syndrome;
 KW inflammatory cachexia; hyperthyroidism; denervation atrophy;
 KW protein/tissue wasting; energy-protein malnutrition; muscle atrophy;
 KW Gene therapy; ss; primer; PCR; primer #2294-37.

XX Homo sapiens.
 OS
 PN US2004185037-A1.
 XX
 PD 23-SEP-2004.
 XX
 PF 15-JAN-2004; 2004US-00758672.
 XX
 PR 08-MAR-2000; 2000US-0187911P.
 PR 28-NOV-2000; 2000US-00724126.
 XX
 PA (HANH/) HAN H.
 PA (KWAK/) KWAK K.
 XX
 PI Han H, Kwak K;
 XX
 WIPI; 2004-707854/69.
 XX
 PT Novel isolated human E3alpha ubiquitin ligase nucleic acid molecule
 PT useful for treating and/or preventing renal cachexia or inflammatory
 PT cachexia.

XX Example 1; SEQ ID NO 10; 115pp; English.
 XX
 CC The present invention relates to new orthologue of human E3alpha
 CC ubiquitin ligase, huE3alphaI and huE3alphaII. Most intracellular
 CC are degraded through the ubiquitin-proteasome pathway. Proteins are
 CC marked for proteasomal degradation by conjugation of ubiquitin to the
 CC protein. Conjugation of the ubiquitin molecule involves the activation by
 CC E1 enzyme, subsequent transfer to E2 enzyme, which serves as a carrier,
 CC and then interacts with a specific E3 ligase family member. E3 ligase
 CC binds to proteins targeted for degradation and catalyses the transfer of
 CC ubiquitin from the E2 carrier enzyme to the target protein. E3 ligase
 CC determines the specificity of the system. The E3alpha family is the main
 CC family of intracellular ligases and is involved in the N-end rule pathway
 CC of protein degradation. E3alpha enzyme binds directly to the primary
 CC destabilising N-terminal amino acid and catalyses ubiquitin conjugation

CC thereby targeting the protein for degradation. The human E3alpha gene is
 CC located on chromosome 15 q. Increased proteolysis through the ubiquitin-
 CC proteasome pathway has been determined to be a major cause of rapid
 CC muscle wasting including, fasting, metabolic acidosis, muscle
 CC degeneration, kidney failure, renal cachexia, uremia, diabetes mellitus,
 CC sepsis, AIDS wasting syndrome, cancer cachexia, inflammatory cachexia,
 CC hyperthyroidism, denervation atrophy, protein/tissue wasting, and energy-
 CC protein malnutrition. E3alpha plays a role in the overall increase in
 CC ubiquitination that is associated with and may mediate muscle atrophy in
 CC cachexia and other disease states. Treatment may be administered by gene
 CC therapy, cell therapy and antisense therapy methods. The present sequence
 CC is primer #2294-37 for PCR of the huE3alphaI gene including the 5' and 3',
 CC untranslated regions.

SQ Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 45.8%; Score 11; DB 13; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCT 21
 |||||
 Db 23 TTCTGAGGGCT 13

RESULT 12
 ADZ75830/c
 ID ADZ75830 standard; DNA; 23 BP.
 XX
 AC ADZ75830;
 DT 14-JUL-2005 (first entry)
 XX
 DE Human E3alphaI cloning PCR primer, 2294-37, SEQ ID NO: 10.
 XX
 KW Gene therapy; diagnosis; ubiquitin ligase; PCR; primer; ss.

XX Homo sapiens.
 OS
 PN US2005089876-A1.
 XX
 PD 28-APR-2005.
 XX
 PF 15-JAN-2004; 2004US-00758636.
 XX
 PR 08-MAR-2000; 2000US-0187911P.
 PR 28-NOV-2000; 2000US-00724126.
 XX
 PA (HANH/) HAN H.
 PA (KWAK/) KWAK K.
 XX
 PI Han H, Kwak K;
 XX
 WIPI; 2005-314084/32.

XX New isolated nucleic acid molecules encoding human E3alpha ubiquitin
 XX ligase polypeptides, useful for diagnosing, preventing or treating
 XX diseases associated with the polypeptides, e.g. conditions involving
 XX muscle atrophy.

XX Example 1; SEQ ID NO 10; 113pp; English.
 XX
 CC The present invention relates to human E3alpha ubiquitin ligase
 CC polypeptides (huE3alphaI and huE3alphaII) and their encoding
 CC polynucleotides. The invention is useful for diagnosing, preventing and
 CC treating diseases associated with huE3alpha polypeptides as well as
 CC methods for identifying modulators of huE3alpha ligase activity. The
 CC invention is also useful in gene therapy. The present sequence is the
 CC human E3alpha ubiquitin ligase I cloning PCR primer.

XX Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

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Query Match      45.8%; Score 11; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TTCTGAGGGCT 21
DB 23 TTCTGAGGGCT 13

RESULT 13
AAL51429/C
ID AAL51429 standard; DNA; 24 BP.
XX AC AAL51429;
XX DT 03-APR-2003 (first entry)
XX DE Human cytoskeleton relative protein 11-33 PCR primer #1.
XX KW Human; ss; cytoskeleton relative protein; 11.33; malignant tumour;
XX KW haemopathy; HIV; immunological disease; inflammation; PCR; primer.
XX OS Homo sapiens.
XX CN1364801-A.
XX 21-AUG-2002.
XX PF 10-JAN-2001; 2001CN-00105178.
XX PR 10-JAN-2001; 2001CN-00105178.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2003-000513/01.
XX New polypeptide-human cytoskeleton relative protein 11.33 and
PT polynucleotide for encoding such polypeptide.
XX Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX The invention comprises the amino acid and coding sequence of the human
CC cytoskeleton relative protein 11.33. The DNA and protein sequences of the
CC invention are useful for treating: malignant tumours; haemopathy; HIV
CC infection; immunological diseases; and inflammations. The present DNA
CC sequence represents a PCR primer for the human cytoskeleton relative
CC protein 11.33 coding sequence
XX
SQ Sequence 24 BP; 7 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      45.8%; Score 11; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TTCTGAGGGCT 21
DB 15 TTCTGAGGGCT 5

RESULT 14
AAT86564
ID AAT86564 standard; DNA; 22 BP.
XX AC AAT86564;
XX DT 24-MAR-1998 (first entry)
XX DE Primer to amplify clone 2.116 containing DNA enriched in triplet repeats.
XX KW Triplet repeat; transcribed DNA; trinucleotide repeat disease;
XX KW myotonic dystrophy; Parkinson's disease; PCR; primer; ss.

Query Match      41.7%; Score 10; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CTGAGGGCTT 22
DB 4 CTGAGGGCTT 13

RESULT 15
AAX09818
ID AAX09818 standard; DNA; 22 BP.
XX AC AAX09818;
XX DT 24-MAR-1999 (first entry)
XX DE Human biallelic polymorphic marker downstream primer #124.
XX KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
XX KW detection; phenotypic typing; characteristic; infection; hereditary;
XX KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX KW treatment; marker; primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX WO9820165-A2.
XX PD 14-MAY-1998.
XX PF 05-NOV-1997; 97WO-US020313.
XX PR 06-NOV-1996; 96US-0030455P.

PCR primers AAT86563-80 were used to amplify nine specific transcribed
DNAs (sequences not given in the specification), enriched in the triplets
CAG or CTG, and their normal or mutated alleles, or complementary
sequences. Sequence comparison between patient DNA and these specific DNA
sequences is used to assess the risk of development of a trinucleotide
repeat disease, i.e. spinobulbar muscular dystrophy; myotonic dystrophy
; cerebrosplinal ataxia; dentato-rubropallidolysian atrophy or
CC Huntington's disease, although many other diseases (e.g. schizophrenia,
CC autism, Parkinson's disease, obsessive disorders) may also be caused by
CC such repeats. The presence of additional triplets indicates risk of
CC disease and the number of extra triplets allows estimation of the age at
CC which the disease will develop and its severity
XX
SQ Sequence 22 BP; 4 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

Query Match      41.7%; Score 10; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CTGAGGGCTT 22
DB 4 CTGAGGGCTT 13

RESULT 15
AAX09818
ID AAX09818 standard; DNA; 22 BP.
XX AC AAX09818;
XX DT 24-MAR-1999 (first entry)
XX DE Human biallelic polymorphic marker downstream primer #124.
XX KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
XX KW detection; phenotypic typing; characteristic; infection; hereditary;
XX KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX KW treatment; marker; primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX WO9820165-A2.
XX PD 14-MAY-1998.
XX PF 05-NOV-1997; 97WO-US020313.
XX PR 06-NOV-1996; 96US-0030455P.

New human transcribed DNA sequences enriched in triplet repeats - used
for treating trinucleotide repeat diseases or assessing the risk of
their development e.g. myotonic dystrophy, Parkinson's disease, etc.

Claim 5; Page 11; 26pp; French.

New human transcribed DNA sequences enriched in triplet repeats - used
for treating trinucleotide repeat diseases or assessing the risk of
their development e.g. myotonic dystrophy, Parkinson's disease, etc.

Claim 5; Page 11; 26pp; French.

PCR primers AAT86563-80 were used to amplify nine specific transcribed
DNAs (sequences not given in the specification), enriched in the triplets
CAG or CTG, and their normal or mutated alleles, or complementary
sequences. Sequence comparison between patient DNA and these specific DNA
sequences is used to assess the risk of development of a trinucleotide
repeat disease, i.e. spinobulbar muscular dystrophy; myotonic dystrophy
; cerebrosplinal ataxia; dentato-rubropallidolysian atrophy or
CC Huntington's disease, although many other diseases (e.g. schizophrenia,
CC autism, Parkinson's disease, obsessive disorders) may also be caused by
CC such repeats. The presence of additional triplets indicates risk of
CC disease and the number of extra triplets allows estimation of the age at
CC which the disease will develop and its severity
XX
SQ Sequence 22 BP; 4 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
```

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA Lander ES, Wang D, Hudson T;
XX WPI; 1998-286974/25.
XX
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
XX Claim 16; Page 60; 310pp; English.
XX
XX AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AAX10269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 22 BP; 9 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 41.7%; Score 10; DB 2; Length 22;
Best Local Similarity 100.0%; Pred.No. 5.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGTTCTGAGG 18
| | | | | | | | | |
Db 2 GGTTCTGAGG 11

Search completed: December 12, 2005, 02:27:51
Job time : 271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:07:58 ; Search time 1927 Seconds
(without alignments)
582.714 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tcgcgagcgttcttgagggttacc 24

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues
Word size : 0
Total number of hits satisfying chosen parameters: 9906

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsal:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	9	37.5	24	CB843231	M15E-4025
2	8	33.3	22	AA938474	CO56H02.S
3	8	33.3	22	AW249729	2B19657.3
4	8	33.3	22	AZ476175	IM0294E14
5	8	33.3	22	AZ788615	2M0035F19
6	8	33.3	22	AZ809838	2M0074G04
7	8	33.3	22	AG203045	Pan trogl
8	8	33.3	22	AL476704	T. brucei
9	8	33.3	22	AL485077	T. brucei
10	8	33.3	22	TA314H07Q	T. brucei
11	8	33.3	23	CO778596	BL004B.B0
12	8	33.3	23	AZ797023	2M0053F06
13	8	33.3	23	AG193857	Pan trogl
14	8	33.3	23	AL477466	T. brucei
15	8	33.3	24	AZ784263	2M0026I19
16	7	29.2	22	AA926856	cm07f06.s
17	7	29.2	22	BX565934	BX565934
18	7	29.2	22	CF330336	NACL--06-
19	7	29.2	22	AZ311109	IM0026E21
20	7	29.2	22	AZ318102	IM0037J11
21	7	29.2	22	AZ407386	IM0178K06
22	7	29.2	22	AZ505531	IM0346F13

C 23	7	29.2	22	9	AZ776605	2M0010I19
24	7	29.2	22	9	AZ806134	2M0068D05
C 25	7	29.2	22	9	AZ861877	2M0168G07
C 26	7	29.2	22	9	BH852180	SALK_0742
C 27	7	29.2	22	10	AJ587479	Arabidops
C 28	7	29.2	22	10	AJ590848	Arabidops
C 29	7	29.2	22	10	CL653644	PR10119a
C 30	7	29.2	22	10	CL660428	PR10137a
C 31	7	29.2	22	11	TA327G01Q	AL493268 T. brucei
C 32	7	29.2	23	1	AJ651207	AJ651207
C 33	7	29.2	23	1	AJ801164	AJ801164
C 34	7	29.2	23	3	BM397206	5009-0-3-
C 35	7	29.2	23	6	CF326961	NACL--01-
C 36	7	29.2	23	7	CK812850	Rasgsc197
C 37	7	29.2	23	9	AZ380370	IM0136G15
C 38	7	29.2	23	9	AZ475927	IM0294B21
C 39	7	29.2	23	9	AZ622587	IM0459F02
C 40	7	29.2	23	9	AZ785027	2M0028H03
C 41	7	29.2	23	9	AZ789956	2M0038L05
C 42	7	29.2	23	11	TA120H10P	AL462505 T. brucei
C 43	7	29.2	23	11	TA338E01P	AL493153 T. brucei
C 44	7	29.2	24	1	AU258060	AU258060
C 45	7	29.2	24	1	AU260297	AU260297

ALIGNMENTS

RESULT 1
CB843231
LOCUS M15E-4025 MOUSE EMBRYONIC DAY 15.5 EYE Mus musculus CDNA 5', mRNA linear EST 25-AUG-2004
DEFINITION sequence.
ACCESSION CB843231
VERSION CB843231.2 GI:515550363
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and Swaroop,A.
AUTHORS Annotation and analysis of 10,000 expressed sequence tags from developing mouse eye and adult retina
JOURNAL Genome Biol. 4 (10), R65 (2003)
PUBMED 14519200
COMMENT On Sep 1, 2003 this sequence version replaced gi:34374345.
Contact: Swaroop, A.
Department of Ophthalmology and Visual Sciences
Kellogg Eye Center, University of Michigan
540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
Tel: 734 615 2246
Fax: 734 647 0228
Email: swaroop@umich.edu.
FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="eye"
/clone_lib="MOUSE EMBRYONIC DAY 15.5 EYE"
/note="Vector: pSPORT1"

ORIGIN
Query Match 37.5%; Score 9; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGGTTCTGA 16
|||||||
DB 10 CGGTTCTGA 18

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RESULT 2
AA938474/c
LOCUS
DEFINITION
AA938474.1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570227 3'
similar to TR:Q92555 MYELOBLAST KIAA0266.1, mRNA sequence.
ACCESSION
AA938474
VERSION
AA938474.1 GI:3096513
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amergham
High quality sequence stop: 1.
FEATURES
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1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1570227"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 33.3%; Score 8; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 GAGGGCTT 22
|||||
Db 14 GAGGGCTT 7
RESULT 3
AW249729
LOCUS
DEFINITION
AW249729.1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570227 3'
similar to TR:Q92555 MYELOBLAST KIAA0266.1, mRNA sequence.
ACCESSION
AW249729
VERSION
AW249729.1 GI:6592722
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```

```

REFERENCE
1 (bases 1 to 22)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Other ESTs: 2819657.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross_match from University of Washington Genome Center
PRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu/LowQuality Sequence: 11
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 22 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L1CM2 row: C column: 18
High quality sequence stop: 11.
FEATURES
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1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819657"
/tissue_type="small cell carcinoma"
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/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies). "
ORIGIN
Query Match 33.3%; Score 8; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAGAC 8
|||||
Db 10 TCCGAGAC 17
RESULT 4
AA2476175
LOCUS
DEFINITION
AA2476175.1 Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0294E14 R, genomic survey sequence.
ACCESSION
AA2476175
VERSION
AA2476175.1 GI:10634300
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Murinae; Mus.
REFERENCE
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

```

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0294 row: E column: 14
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES source

1. .22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0294E14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 33.3%; Score 8; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.5e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGG 19
 |||||
 Db 12 TCTGAGGG 19

RESULT 5
 AZ788615
 LOCUS AZ788615
 DEFINITION 2M0035F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035F19 R, genomic survey sequence.
 ACCESSION AZ788615
 VERSION AZ788615.1 GI:12928595
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: F column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES source

1. .22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0035F19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 33.3%; Score 8; DB 9; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.5e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCT 21
 |||||
 Db 5 TGAGGGCT 12

RESULT 6
 AZ809838/c
 LOCUS AZ809838
 DEFINITION 2M0074G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074G04 F, genomic survey sequence.
 ACCESSION AZ809838
 VERSION AZ809838.1 GI:12976504
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE
JOURNAL
COMMENT

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: dduwn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: G column: 04

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0074G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 33.3%; Score 8; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGG 19

Db 9 TCTGAGGG 2
|||||

RESULT 7

AG203045

LOCUS

AG203045 22 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-087A06.T7, genomic survey
sequence.

ACCESSION AG203045

VERSION AG203045.1 GI:45235220

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE

AUTHORS

Park,H., Kim,X., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 22)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

source

1. .22

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-087A06.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 33.3%; Score 8; DB 10; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.5e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCT 21

|||||

Db 8 TGAGGGCT 15

RESULT 8

TA207D04P

LOCUS

TA207D04P 22 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 207d04, forward sequence,
genomic survey sequence.

ACCESSION AL476704.1 GI:11843292

VERSION GSS.

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 22)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/. Location/Qualifiers		T. brucei sheared genomic DNA clone 314h07, reverse sequence, genomic survey sequence.	
FEATURES	source	1. .22	
		/organism="Trypanosoma brucei"	
		/mol_type="genomic DNA"	
		/strain="TREU927"	
		/db_xref="taxon:5691"	
		/clone="207d04"	
ORIGIN		Trypanosomatidae;	
Query Match		33.3%;	Score 8; DB 11; Length 22;
Best Local Similarity		100.0%;	Pred. No. 4.5e+06;
Matches	8;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	7	ACGGTTCT 14	
Db	3	ACGGTTCT 10	
RESULT 9		TA294D03P	
LOCUS		22 bp DNA linear	GSS 13-DEC-2000
DEFINITION		T. brucei sheared genomic DNA clone 294d03, forward sequence, genomic survey sequence.	
ACCESSION		AL485077	
VERSION		AL485077.1	GI:11852827
KEYWORDS		GSS.	
SOURCE	Trypanosoma brucei	Trypanosomatidae;	
ORGANISM	Trypanosoma brucei	Trypanosomatidae;	
REFERENCE		1 (bases 1 to 22)	
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajadream,M.A. and Barrell,B.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk		
COMMENT		Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	
Email: nelsayed@tigr.org			
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.			
Location/Qualifiers			
FEATURES	source	1. .22	
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		/strain="TREU927"	
		/db_xref="taxon:5691"	
		/clone="294d03"	
ORIGIN		Trypanosomatidae;	
Query Match		33.3%;	Score 8; DB 11; Length 22;
Best Local Similarity		100.0%;	Pred. No. 4.5e+06;
Matches	8;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	3	CGAGACGG 10	
Db	5	CGAGACGG 12	
RESULT 10		TA314H07Q	
LOCUS		22 bp DNA linear	GSS 13-DEC-2000

T. brucei sheared genomic DNA clone 314h07, reverse sequence, genomic survey sequence.		23 bp mRNA linear EST 05-AUG-2004	
ACCESSION	AL489914	BL004B_B06	6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
VERSION	AL489914.1	CDNA	5' similar to hypothetical protein, mRNA sequence.
KEYWORDS	GSS.		
SOURCE	Trypanosoma brucei		
ORGANISM	Trypanosoma brucei		
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;		
Trypanosoma.			
1 (bases 1 to 22)			
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajadream,M.A. and Barrell,B.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk		
COMMENT		Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	
Email: nelsayed@tigr.org			
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.			
Location/Qualifiers			
FEATURES	source	1. .22	
		/organism="Trypanosoma brucei"	
		/mol_type="genomic DNA"	
		/strain="TREU927"	
		/db_xref="taxon:5691"	
		/clone="314h07"	
ORIGIN		Trypanosomatidae;	
Query Match		33.3%;	Score 8; DB 11; Length 22;
Best Local Similarity		100.0%;	Pred. No. 4.5e+06;
Matches	8;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	11	TTCTGAGG 18	
Db	3	TTCTGAGG 10	
RESULT 11		CO778596	
LOCUS		23 bp	mRNA linear EST 05-AUG-2004
DEFINITION		BL004B_B06 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum cDNA 5' similar to hypothetical protein, mRNA sequence.	
ACCESSION		CO778596	
VERSION		CO778596.1	GI:50994576
KEYWORDS		EST.	
SOURCE	Ambystoma mexicanum (axolotl)	Ambystomidae;	
ORGANISM	Ambystoma mexicanum	Ambystomidae;	
REFERENCE		1 (bases 1 to 23)	
AUTHORS	Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K., Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.		
TITLE	An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries		
JOURNAL	Genome Biol. (2004) In press		
COMMENT	Contact: Elly M. Tanaka Tanaka Lab Max Planck Institute of Molecular Cell Biology and Genetics, Dresden Pfotenauerstrasse 108,01307 Dresden,Germany		

Tel: 0049 351 210 2620
 Fax: 0049 351 210 1489
 Email: tanaka@mpi-cbg.de
 Plate: BL004B row: 06 column: B
 Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
 Location/Qualifiers

FEATURES

source

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1..23
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
/note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 KB.
TAG_LIFB=6DaxBL"
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ORIGIN

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Query Match      33.3%; Score 8; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAGACGGT 11
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Db 14 GAGACGGT 21

RESULT 12
AZ797023/c
LOCUS          23 bp DNA linear GSS 16-FEB-2001
DEFINITION     clone U062M0053F06 F, genomic survey sequence.
ACCESSION      AZ797023
VERSION        AZ797023.1 GI:12945674
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Ross,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0053 row: F column: 06
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0053F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
```

```
/clone_lib="Mouse 10kb plasmid U062M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ORIGIN

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Query Match      33.3%; Score 8; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.5e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGGTTCT 14
    |||||
Db 23 ACGGTTCT 16

RESULT 13
AG193857/c
LOCUS          23 bp DNA linear GSS 06-MAR-2004
DEFINITION     Pan troglodytes DNA, clone: RP43-071F16.T7, genomic survey
sequence.
ACCESSION      AG193857
VERSION        AG193857.1 GI:45226033
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
ORGANISM       Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pan.
1
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 23)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : DBACE3.6
R.Site 1 : ECORI
R.Site 2 : ECORI
Location/Qualifiers
1..23
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-071F16.T7"
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FEATURES

source

ORIGIN	/sex="male"				SOURCE	Mus musculus (house mouse)
	/cell_type="lymphocytes"					Mus musculus
	/clone_lib="RP-43 Chimpanzee Male BAC Library"					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Query Match	33.3%;	Score 8;	DB 10;	Length 23;	REFERENCE	1 (bases 1 to 24)
Best Local Similarity	100.0%;	Pred. No. 4.5e+06;			AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0;	TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
QY	14	TGAGGGCT	21		JOURNAL	Unpublished (2000)
Db	18	TGAGGGCT	11		COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0026 row: 1 column: 19 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 24.
RESULT 14	TA201E03Q 23 bp DNA linear GSS 13-DEC-2000				FEATURES	Location/Qualifiers
LOCUS	T. brucei sheared genomic DNA Clone 201e03, reverse sequence, genomic survey sequence.				source	1. .24
DEFINITION	AL477466					/organism="Mus musculus"
ACCESSION	AL477466.1 GI:11843747					/mol_type="genomic DNA"
VERSION	GSS.					/strain="C57BL/6J"
KEYWORDS	Trypanosoma brucei					/db_xref="taxon:10090"
SOURCE	Trypanosoma brucei					/clone="UUGC2M0026119"
ORIGIN	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.					/sex="Male"
REFERENCE	1 (bases 1 to 23)					/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.					/clone_lib="Mouse 10kb plasmid UUGC1M library"
TITLE	Direct Submission					/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk					
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/. Location/Qualifiers					
FEATURES	1. .23					
source	/organism="Trypanosoma brucei"					
	/mol_type="genomic DNA"					
	/strain="TREU927"					
	/db_xref="taxon:5691"					
	/clone="201e03"					
ORIGIN	33.3%; Score 8; DB 11; Length 23;				ORIGIN	33.3%; Score 8; DB 9; Length 24;
Query Match	33.3%;	Score 8;	DB 11;	Length 23;	Query Match	33.3%;
Best Local Similarity	100.0%;	Pred. No. 4.5e+06;			Best Local Similarity	100.0%;
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	17	GGGCTTAC	24		QY	7 ACGTTTCT 14
Db	3	GGGCTTAC	10		Db	16 ACGTTTCT 23
RESULT 15	AZ784263 24 bp DNA linear GSS 16-FEB-2001					
LOCUS	2M0026119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic					
DEFINITION	Clone UUGC2M0026119 R, genomic survey sequence.					
ACCESSION	AZ784263					
VERSION	AZ784263.1 GI:12919809					
KEYWORDS	GSS.					
Query Match	33.3%;	Score 8;	DB 11;	Length 23;		
Best Local Similarity	100.0%;	Pred. No. 4.5e+06;				
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0;		
QY	17	GGGCTTAC	24			
Db	3	GGGCTTAC	10			
RESULT 16	AZ784263 24 bp DNA linear GSS 16-FEB-2001					
LOCUS	2M0026119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic					
DEFINITION	Clone UUGC2M0026119 R, genomic survey sequence.					
ACCESSION	AZ784263					
VERSION	AZ784263.1 GI:12919809					
KEYWORDS	GSS.					
Query Match	33.3%;	Score 8;	DB 9;	Length 24;		
Best Local Similarity	100.0%;	Pred. No. 4.5e+06;				
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0;		
QY	7	ACGTTTCT	14			
Db	16	ACGTTTCT	23			
Search completed:	December 12, 2005, 03:28:25					
Job time :	1930 secs					

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:19:42 ; Search time 93 Seconds
(without alignments)
458.726 Million cell updates/sec

Title: US-10-688-489-74

Perfect score: 24

Sequence: 1 tcgagacggttctgagggttac 24

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 107492

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*

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- 2: /cgn2_6/prodata/1/ina/5_COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/ECTUS_COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP_COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	50.0	22	3	US-09-332-522E-65
C 2	11	45.8	23	3	US-09-724-126A-10
C 3	10	41.7	22	3	US-08-943-731-438
C 4	10	41.7	22	3	US-09-159-871-10
C 5	10	41.7	23	2	US-08-859-998-816
C 6	10	41.7	23	3	US-08-989-394-19
C 7	10	41.7	23	3	US-09-271-365-19
C 8	10	41.7	23	3	US-09-018-584A-100
C 9	10	41.7	23	3	US-09-225-928-816
C 10	10	41.7	23	3	US-09-604-013A-19
C 11	10	41.7	23	3	US-09-225-201B-816
C 12	10	41.7	23	3	US-09-784-423-100
C 13	10	41.7	23	3	US-10-192-369-3
C 14	10	41.7	23	3	US-10-192-085-19
C 15	10	41.7	24	2	US-08-691-814B-68
C 16	10	41.7	24	3	US-09-538-709-235
C 17	10	41.7	24	3	US-09-930-803-14
C 18	10	41.7	24	3	US-09-521-195B-25
C 19	10	41.7	24	3	US-09-798-743-25
C 20	9	37.5	22	2	US-08-139-540-1
C 21	9	37.5	22	2	US-08-197-791-24
C 22	9	37.5	22	2	US-08-634-826-1
C 23	9	37.5	22	3	US-09-115-175-1
C 24	9	37.5	22	3	US-09-150-805-6

ALIGNMENTS

RESULT 1

US-09-332-522E-65/c
; Sequence 65, Application US/09332522E
; Patent No. 6781028
; GENERAL INFORMATION:
; APPLICANT: Costa, M.
; APPLICANT: Doberstein, S.
; APPLICANT: Elson, S. S.
; APPLICANT: Ferguson, K.
; APPLICANT: Homberger, S.
; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND
; FILE REFERENCE: 7326-101, EX99-004
; CURRENT APPLICATION NUMBER: US/09/332,522E
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-332-522E-65

Query Match 50.0%; Score 12; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTCTGAGGGCT 21

Db 15 GTTCTGAGGGCT 4

RESULT 2

US-09-724-126A-10/c
; Sequence 10, Application US/09724126A
; Patent No. 6706505
; GENERAL INFORMATION:
; APPLICANT: Han, Hui-Quan
; APPLICANT: Kwak, Keith
; TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
; FILE REFERENCE: 01017/35966A
; CURRENT APPLICATION NUMBER: US/09/724,126A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,211
; PRIOR FILING DATE: 1999-03-01

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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer 2294-37
US-09-724-126A-10

Query Match          45.8%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTCTGAGGCGCT 21
Db 23 TTCTGAGGCGCT 13

RESULT 3
US-08-943-731-438
; Sequence 438, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-963-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 438:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-438

Query Match          41.7%; Score 10; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGTCTGAGG 18
Db 11 GGTCTGAGG 20

RESULT 4
US-09-159-871-10/c
; Sequence 10, Application US/09159871A
; Patent No. 6420136
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
; FILE REFERENCE: 028722-181
; CURRENT APPLICATION NUMBER: US/09/159,871A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/060,138
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: US 09/006,783
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Human
US-09-159-871-10

Query Match          41.7%; Score 10; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GAGGCGCTTAC 24
Db 19 GAGGCGCTTAC 10

RESULT 5
US-08-859-998-816/c
; Sequence 816, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
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41.7%; Score 10; DB 2; Length 23;

US-08-859-998-816

41.7%; Score 10; DB 2; Length 23;

US-09-271-365-19

TITLE OF INVENTION: MATERIALS AND

US-09-271-365-19

TITLE OF INVENTION: MATERIALS AND

;; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
;; TITLE OF INVENTION: REPEAT DNA MARKERS
;; NUMBER OF SEQUENCES: 147
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Promega Corporation
;; STREET: 2800 Woods Hollow Road
;; CITY: Madison
;; STATE: Wisconsin
;; COUNTRY: U.S.A.
;; ZIP: 53711-5399

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
;; COMPUTER: IBM compatible PC
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Word 97 (DOS text format)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/018,584A
;; FILING DATE: 04-Feb-1998
;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Grady J. Frenchick
;; REGISTRATION NUMBER: 29,018
;; REFERENCE/DOCKET NUMBER: 16026.9180
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (608) 257-3501
;; TELEFAX: (608) 257-2275

;; INFORMATION FOR SEQ ID NO: 100:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
US-09-018-584A-100

Query Match 41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22
Db 11 CTGAGGGCTT 20

RESULT 9

US-09-225-928-816/c
; Sequence 816, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jekhade, George
; Bibilashvili, Robert

;; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;; EXPRESSION

;; NUMBER OF SEQUENCES: 1375
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 2200 Sand Hill Road, Suite 100
;; CITY: Menlo Park
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94025

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/225,928
;; FILING DATE: 05-Jan-1999
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/859,998
;; FILING DATE: 21-MAY-1997

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Field, Bret E.
;; REGISTRATION NUMBER: 37,620
;; REFERENCE/DOCKET NUMBER: 09096/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-322-5070
;; TELEFAX: 415-854-0875

;; INFORMATION FOR SEQ ID NO: 816:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide primer
US-09-225-928-816

Query Match 41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACGGTTCT 14
Db 19 AGACGGTTCT 10

RESULT 10

US-09-604-013A-19/c
; Sequence 19, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dull, Thomas
; Farson, Deborah A.
; Witt, Rochelle

;; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;; TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS

;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;; STREET: 2100 Pennsylvania Avenue, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20037

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/604,013A
;; FILING DATE: 26-Jun-2000
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/271,365
;; FILING DATE: 18-Mar-1999
;; APPLICATION NUMBER: 08/989,394
;; FILING DATE: 12-DEC-1997

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Nakamura, Dean H.
;; REGISTRATION NUMBER: 33,981
;; REFERENCE/DOCKET NUMBER: A7086
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)293-7060
;; TELEFAX: (202)293-7860

;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-604-013A-19

Query Match          41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21
Db 21 TCTGAGGGCT 12

RESULT 11
US-09-225-201B-816/c
; Sequence 816, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Bibilashvili, Robert
; Jokhadze, George
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 816:
US-09-225-201B-816

Query Match          41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACGGTTCT 14
Db 19 AGACGGTTCT 10

RESULT 12
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US-09-784-423-100
; Sequence 100, Application US/09784423
; Patent No. 6767703
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 100
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100
US-09-784-423-100

Query Match          41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22
Db 11 CTGAGGGCTT 20

RESULT 13
US-10-192-369-3/c
; Sequence 3, Application US/10192369
; Patent No. 6797464
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Mario
; APPLICANT: Sharkey, Mark
; TITLE OF INVENTION: DETECTION OF DRUG-RESISTANT HUMAN
; IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 07917-163001
; CURRENT APPLICATION NUMBER: US/10/192,369
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: synthetic probe
US-10-192-369-3

Query Match 41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred.No. 1e+04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 12 TCTGAGGGCT 21
Db 17 TCTGAGGGCT 8

RESULT 14

US-10-192-085-19/c
; Sequence 19, Application US/10192085
; Patent No. 6924144

GENERAL INFORMATION:

APPLICANT: Naldini, Luigi
Dull, Thomas
Farson, Deborah A.
Witt, Rochelle

TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
CORRESPONDENCE ADDRESS:

ADDRESS: SUHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/192,085
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-192-085-19

Query Match 41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred.No. 1e+04; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 12 TCTGAGGGCT 21
Db 21 TCTGAGGGCT 12

RESULT 15

US-08-691-814B-68/c

; Sequence 68, Application US/08691814B
; Patent No. 5981218

GENERAL INFORMATION:

APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Basset, Paul
APPLICANT: Byrne, Jennifer

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
as Leukemia Markers and in Breast Cancer Prognosis
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-691-814B-68

Query Match 41.7%; Score 10; DB 2; Length 24;

Best Local Similarity 100.0%; Pred.No. 1e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTGAGGGCT 21

Db 19 TCTGAGGGCT 10

Search completed: December 12, 2005, 03:30:02

Job time : 94 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:56:14 ; Search time 421 Seconds
(without alignments)
471.413 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggtttac 24

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 268506

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : Published Applications NA.Main:*

- 1: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/us09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/us09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/us10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/us10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/us10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/us10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/us10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-10-688-489-74
2	24	100.0	24	8	US-10-688-489-74
3	23	95.8	22	8	US-10-688-489-75
4	22	91.7	22	8	US-10-688-489-76
5	21	87.5	23	8	US-10-688-489-77
6	11	45.8	23	8	US-10-688-489-149
7	11	45.8	23	9	US-10-758-672A-10
8	10	41.7	22	7	US-10-758-636A-10
9	10	41.7	22	7	US-10-114-270-273
10	10	41.7	22	9	US-10-477-166-10
11	10	41.7	22	9	US-10-887-553A-63
12	10	41.7	23	3	US-09-784-423-100
13	10	41.7	23	3	US-09-750-410-47
14	10	41.7	23	5	US-10-192-085-19
15	10	41.7	23	6	US-10-192-369-3
16	10	41.7	23	8	US-10-712-642-47
17	10	41.7	23	9	US-10-795-580-3
18	10	41.7	23	9	US-10-825-593-108
19	10	41.7	24	3	US-09-798-743A-25
20	10	41.7	24	3	US-09-940-185-3550
21	10	41.7	24	5	US-10-154-971-5
22	10	41.7	24	6	US-10-323-463-15
23	10	41.7	24	6	US-10-403-107-14
24	10	41.7	24	8	US-10-762-154-25

C 24	10	41.7	24	8	US-10-940-500-25	Sequence 25, Appl
C 25	10	41.7	24	9	US-10-257-158A-1254	Sequence 1254, Ap
C 26	10	41.7	24	9	US-10-257-158A-2822	Sequence 2822, Ap
C 27	10	41.7	24	9	US-10-257-158A-3501	Sequence 3501, Ap
C 28	9	37.5	22	3	US-09-755-665-77	Sequence 77, Appl
C 29	9	37.5	22	3	US-09-796-599-1	Sequence 1, Appl
C 30	9	37.5	22	3	US-09-745-008-25	Sequence 25, Appl
C 31	9	37.5	22	3	US-09-729-653-5	Sequence 5, Appl
C 32	9	37.5	22	3	US-09-938-689-52	Sequence 52, Appl
C 33	9	37.5	22	3	US-09-944-161-10	Sequence 10, Appl
C 34	9	37.5	22	3	US-09-840-743-77	Sequence 77, Appl
C 35	9	37.5	22	5	US-10-138-316-46	Sequence 46, Appl
C 36	9	37.5	22	5	US-10-153-219-26	Sequence 26, Appl
C 37	9	37.5	22	6	US-10-093-626B-56	Sequence 56, Appl
C 38	9	37.5	22	6	US-10-309-814-1	Sequence 1, Appl
C 39	9	37.5	22	6	US-10-368-643-46	Sequence 46, Appl
C 40	9	37.5	22	6	US-10-313-669-292	Sequence 292, Appl
C 41	9	37.5	22	7	US-10-203-516A-5	Sequence 5, Appl
C 42	9	37.5	22	7	US-10-203-516A-6	Sequence 6, Appl
C 43	9	37.5	22	7	US-10-037-417-185	Sequence 185, Appl
C 44	9	37.5	22	7	US-10-380-614-10	Sequence 10, Appl
C 45	9	37.5	22	7	US-10-456-848-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-74

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTAC 24
Db 1 TCCGAGACGGTTCGAGGGCTTAC 24

RESULT 2
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-75
```

```
Query Match          100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TCCGAGACGGTTCTGAGGCGCTTAC 24
|||||
Db 1 TCCGAGACGGTTCTGAGGCGCTTAC 24
```

RESULT 3

```
US-10-688-489-76
; Sequence 76, Application US/10688489
; Publication No. US20040259108A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 23
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-76
```

```
Query Match          95.8%; Score 23; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TCCGAGACGGTTCTGAGGCGCTTA 23
|||||
Db 1 TCCGAGACGGTTCTGAGGCGCTTA 23
```

RESULT 4

```
US-10-688-489-77
; Sequence 77, Application US/10688489
; Publication No. US20040259108A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 22
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-77
```

```
Query Match          91.7%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TCCGAGACGGTTCTGAGGCGCTT 22
|||||
Db 1 TCCGAGACGGTTCTGAGGCGCTT 22
```

RESULT 5

```
US-10-688-489-149
; Sequence 149, Application US/10688489
; Publication No. US20040259108A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 23
; TYPE: RNA
; ORGANISM: West Nile Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: 2'-OME nucleotide analogs
US-10-688-489-149
```

```
Query Match          87.5%; Score 21; DB 8; Length 23;
Best Local Similarity 76.2%; Pred. No. 0.0053;
Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 GAGACGGTTCTGAGGCGCTTAC 24
|||||
Db 1 GAGACGGUUCUGAGGCGCUAC 21
```


RESULT 6

US-10-758-672A-10/c
; Sequence 10, Application US/10758672A
; Publication No. US20040185037A1
; GENERAL INFORMATION:
; APPLICANT: Han, et al.
; TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY
; FILE REFERENCE: 01017/35966B
; CURRENT APPLICATION NUMBER: US/10/758,672A
; CURRENT FILING DATE: 2004-01-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,911
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-758-672A-10

Query Match 45.8%; Score 11; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCT 21
|||||
DB 23 TTCTGAGGGCT 13

RESULT 7

US-10-758-636A-10/c
; Sequence 10, Application US/10758636A
; Publication No. US20050089876A1
; GENERAL INFORMATION:
; APPLICANT: Han, et al.
; TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY
; FILE REFERENCE: 01017/35966C
; CURRENT APPLICATION NUMBER: US/10/758,636A
; CURRENT FILING DATE: 2004-01-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,911
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-758-636A-10

Query Match 45.8%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCTGAGGGCT 21
|||||
DB 23 TTCTGAGGGCT 13

RESULT 8

US-10-114-270-273
; Sequence 273, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:

; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Liu, Ziaohong
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Li, Li
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gorman, Linda
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Smithson, Glenna
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Ji, Weizhen
; APPLICANT: Anderson, David W.
; APPLICANT: Liete, Mario W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: MacDougall, John R.
; APPLICANT: Rothenberg, Mark E.
; TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-322C
; CURRENT APPLICATION NUMBER: US/10/114,270
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 273
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-114-270-273

Query Match 41.7%; Score 10; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22
|||||
DB 5 CTGAGGGCTT 14

RESULT 9

US-10-477-166-10
; Sequence 10, Application US/10477166
; Publication No. US20040234481A1
; GENERAL INFORMATION:
; APPLICANT: ANGES MG, INC.
; APPLICANT: Morishita, Ryuichi
; APPLICANT: Nakanishi, Kuniaki
; APPLICANT: Kaneda, Yasufumi
; APPLICANT: Kotani, Hitoshi
; TITLE OF INVENTION: GENE TRANSFER OF ANGIOGENIC FACTOR FOR SKIN DISEASE
; FILE REFERENCE: 6235-67174
; CURRENT APPLICATION NUMBER: US/10/477,166
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: PCT/JP02/04529
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: JP 2001-139373
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-477-166-10

Query Match 41.7%; Score 10; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21

Db 12 TCTGAGGGCT 21

RESULT 10

US-10-887-553A-63
; Sequence 63, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 22
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(22)
; OTHER INFORMATION: Reverse primer
US-10-887-553A-63

Query Match 41.7%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGAG 17

Db 11 CGGTTCTGAG 20

RESULT 11

US-09-784-423-100
; Sequence 100, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 100
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 100
US-09-784-423-100

Query Match 41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22

Db 11 CTGAGGGCTT 20

RESULT 12

US-09-750-410-47
; Sequence 47, Application US/09750410
; Publication No. US20030083276A1
; GENERAL INFORMATION:
; APPLICANT: Li, Gloria C.
; APPLICANT: Burgman, Paul W.J.J.
; TITLE OF INVENTION: USES OF DNA-PK
; FILE REFERENCE: 1747/55672-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/750,410
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:

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; OTHER INFORMATION: Oligonucleotide Primer
US-09-750-410-47

Query Match          41.7%; Score 10; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22
Db 3 CTGAGGGCTT 12

RESULT 13
US-10-192-085-19/c
; Sequence 19, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dull, Thomas
; Farson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUCHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-192-085-19

Query Match          41.7%; Score 10; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21
Db 21 TCTGAGGGCT 12
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RESULT 14
US-10-192-369-3/c

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; Sequence 3, Application US/10192369
; Publication No. US20040009124A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Mario
; APPLICANT: Sharkey, Mark
; TITLE OF INVENTION: DETECTION OF DRUG-RESISTANT HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 07917-163001
; CURRENT APPLICATION NUMBER: US/10/192,369
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic probe
US-10-192-369-3

Query Match          41.7%; Score 10; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21
Db 17 TCTGAGGGCT 8

RESULT 15
US-10-712-642-47
; Sequence 47, Application US/10712642
; Publication No. US20050032726A1
; GENERAL INFORMATION:
; APPLICANT: Li, Gloria C.
; APPLICANT: Burgman, Paul W.J.J.
; TITLE OF INVENTION: USES OF DNA-PK
; FILE REFERENCE: 1747/55672-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/712,642
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US/09/750,410
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-712-642-47

Query Match          41.7%; Score 10; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCTT 22
Db 3 CTGAGGGCTT 12
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Search completed: December 12, 2005, 04:27:32
Job time : 422 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 21:35:42 ; Search time 62.8364 Seconds
(without alignments)
678.930 Million cell updates/sec

Title: US-10-688-489-74

Perfect score: 24

Sequence: 1 tcgcagacgggtcttgagggtttac 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	16.8	70.0	2799	3	US-08-968-752B-5
2	16.8	70.0	2799	3	US-09-536-224-5
3	16.6	69.2	601	3	US-09-949-016-157466
4	16.6	69.2	601	3	US-09-949-016-157573
5	16.6	69.2	601	3	US-09-949-016-157573
6	16.6	69.2	126176	3	US-09-949-016-16137
7	16.6	69.2	126176	3	US-09-949-016-16138
8	16.6	69.2	153866	3	US-09-949-016-16919
9	16.6	69.2	166698	3	US-09-949-016-16919
10	16.6	69.2	767677	3	US-09-949-016-16138
11	16.6	69.2	767677	3	US-09-949-016-16138
12	16.6	69.2	4403765	3	US-09-103-840A-2
13	16.6	69.2	4411529	3	US-09-103-840A-1
14	16.2	67.5	921	3	US-09-107-532A-2264
15	16.2	67.5	1815	3	US-09-832-496-1
16	16.2	67.5	1815	3	US-09-832-496-1
17	16.2	67.5	21721	3	US-09-269-939A-41
18	16.2	67.5	22976	3	US-09-269-939A-19
19	16.2	67.5	23187	3	US-09-499-522-1
20	16.2	66.7	522	3	US-09-252-991A-8519
21	16.2	66.7	579	3	US-09-270-767-12997
22	16.2	66.7	1113	3	US-09-252-991A-8445
23	16.2	66.7	1850	3	US-09-799-451-367
24	16.2	66.7	2409	3	US-09-252-991A-8479

C 25	16	66.7	7240	3	US-09-695-795A-1	Sequence 1, Appli
C 26	15.8	65.8	37	2	US-08-199-507B-21	Sequence 21, Appl
C 27	15.8	65.8	37	2	US-08-441-828-21	Sequence 21, Appl
C 28	15.8	65.8	601	3	US-09-949-016-192257	Sequence 192257,
C 29	15.8	65.8	1621	2	US-08-292-688A-10	Sequence 10, Appl
C 30	15.8	65.8	1795	2	US-08-791-849A-12	Sequence 12, Appl
C 31	15.8	65.8	55031	3	US-09-949-016-17389	Sequence 17389, A
C 32	15.8	65.8	90776	3	US-09-949-016-17230	Sequence 17230, A
C 33	15.8	65.8	122772	3	US-09-949-016-14132	Sequence 14132, A
C 34	15.8	65.8	767677	3	US-09-949-016-12147	Sequence 12147, A
C 35	15.8	65.8	767677	3	US-09-949-016-17361	Sequence 17361, A
C 36	15.6	65.0	601	3	US-09-949-016-45837	Sequence 45837, A
C 37	15.6	65.0	601	3	US-09-949-016-45859	Sequence 45859, A
C 38	15.6	65.0	948	3	US-09-489-039A-1034	Sequence 1034, Ap
C 39	15.6	65.0	1341	3	US-09-248-796A-6062	Sequence 6062, Ap
C 40	15.6	65.0	2121	3	US-09-902-540-8806	Sequence 8806, Ap
C 41	15.6	65.0	2332	3	US-09-949-016-253	Sequence 253, App
C 42	15.6	65.0	2332	3	US-09-949-016-5522	Sequence 5522, App
C 43	15.6	65.0	3595	3	US-09-949-016-408	Sequence 408, App
C 44	15.6	65.0	3607	3	US-09-563-269-17	Sequence 17, Appl
C 45	15.6	65.0	3943	3	US-08-506-296B-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-08-968-752B-5

; Sequence 5, Application US/08968752B

; Patent No. 6043073

; GENERAL INFORMATION:

; APPLICANT: Frohman, Michael A.

; APPLICANT: Morris, Andrew

; TITLE OF INVENTION: NO. 6043073el Phospholipase D Polypeptide and

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ONYX Pharmaceuticals, Inc.

; STREET: 3031 Research Drive

; CITY: Richmond

; STATE: California

; COUNTRY: USA

; ZIP: 94806

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/968,752B

; FILING DATE: 13-AUG-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/025,469

; FILING DATE: 05-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Giotta, Gregory J.

; REGISTRATION NUMBER: 32,028

; REFERENCE/DOCKET NUMBER: ONYX2004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-222-9700

; TELEFAX: 510-222-9758

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2799 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

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; LOCATION: 1..2799
US-08-968-752B-5

Query Match
Best Local Similarity 70.0%; Score 16.8; DB 3; Length 2799;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGGCT 21
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Db 444 CCGAGAGGTTCTGAGGGCT 463

RESULT 2
US-09-536-224-5
; Sequence 5, Application US/09536224
; Patent No. 6379665
; GENERAL INFORMATION:
; APPLICANT: Frohman, Michael A.
; TITLE OF INVENTION: No. 6379665el Phospholipase D Polypeptide and
; TITLE OF INVENTION: DNA Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/968,752
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory J.
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-222-9700
; TELEFAX: 510-222-9758
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2799
US-09-536-224-5

Query Match
Best Local Similarity 70.0%; Score 16.8; DB 3; Length 2799;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTTCGAGGGCT 21
||||| ||||| ||||| |||||
Db 444 CCGAGAGGTTCTGAGGGCT 463

RESULT 3
US-09-949-016-157466
; Sequence 157466, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157466
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-157466

Query Match
Best Local Similarity 69.2%; Score 16.6; DB 3; Length 601;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTA 23
||||| ||||| ||||| |||||
Db 273 TCAGAGATGATTTTGAGGGCTTA 295

RESULT 4
US-09-949-016-157573
; Sequence 157573, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157573
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-157573

Query Match
Best Local Similarity 69.2%; Score 16.6; DB 3; Length 601;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCGAGGGCTTA 23
||||| ||||| ||||| |||||
Db 273 TCAGAGATGATTTTGAGGGCTTA 295

RESULT 5
US-09-949-016-198733
; Sequence 198733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16138
; LENGTH: 126176
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16138

Query Match          69.2%;      Score 16.6;  DB 3;      Length 126176;
Best Local Similarity 82.6%;      Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DQ **1** TCCGAGACGGTTC TGAGGCCTTA **23**

 ||||| |

Db **72087** TCAGAGATGATTTTGAGGCCTTA **72109**

RESULT 8
US-09-949-016-16919
Seminar 16918, April 23, 2009, 00040012

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16919
; LENGTH: 153866
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16919

Query Match          69.2%; Score 16.6; DB 3; Length 153866;
Best Local Similarity 82.6%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY		2	CCGAGACGGTCTCTGAGGCCTTAC	24
D _b		88075	CCGCCACGATTCTGAGGCCTCC	88097

RESULT 9
US-09-949-016-16038
: Sermonica 16038 Application US/09949012

/ GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16038
; LENGTH: 166698
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(166698)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16038

Query Match          69.2%; Score 16.6; DB 3; Length 166698;
Best Local Similarity 82.6%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTA 23
Db 20937 TCAGAGATGGTTCAGGGGCTGA 20959

RESULT 10
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match          69.2%; Score 16.6; DB 3; Length 767677;
Best Local Similarity 82.6%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTA 23
Db 20937 TCAGAGATGGTTCAGGGGCTGA 20959

RESULT 11
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match          69.2%; Score 16.6; DB 3; Length 767677;
Best Local Similarity 82.6%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTA 23
Db 303242 TCCGTCACGGTTCGGGGGCTGA 303220

RESULT 12
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          69.2%; Score 16.6; DB 3; Length 4403765;
Best Local Similarity 82.6%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCAGGGCTTA 23
Db 2392950 TCCGAGACGGTCCGGGGGCTATA 2392928

RESULT 13
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
```



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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      69.2%; Score 16.6; DB 3; Length 4411529;
Best Local Similarity 82.6%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCGAGGGCTTA 23
Db 2394408 TCCGAGACGGTCCGGCGGCATA 2394386

RESULT 14
US-09-107-532A-2264
; Sequence 2264, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1....921
; SEQUENCE DESCRIPTION: SEQ ID NO: 2264:
US-09-107-532A-2264

Query Match      67.5%; Score 16.2; DB 3; Length 921;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
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Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAGACGGTTCGAGGGCTTAC 24
Db 533 GAGACGGTTATGACGGCTTCC 553

RESULT 15
US-09-832-496-1
; Sequence 1, Application US/09832496
; Patent No. 6503508
; GENERAL INFORMATION:
; APPLICANT: Danielsen, Steffen
; TITLE OF INVENTION: Polypeptides having haloperoxidase activity
; FILE REFERENCE: 10042.200-US
; CURRENT APPLICATION NUMBER: US/09/832,496
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Dreschlera hartleibii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1815)
US-09-832-496-1

Query Match      67.5%; Score 16.2; DB 3; Length 1815;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGACGGTTCGAGGGCTTA 23
Db 1606 CGTGAGGGTTGTGAGGGCTTA 1626

Search completed: December 12, 2005, 00:33:41
Job time : 67.8364 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:28:08 ; Search time 304.582 Seconds
(without alignments)
651.599 Million cell updates/sec

Title: US-10-688-489-74

Perfect score: 24
Sequence: 1 tcgagacgggtcttgagggtttac 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	8	US-10-688-489-74 Sequence 74, Appl
2	24	100.0	24	8	US-10-688-489-74 Sequence 75, Appl
3	24	100.0	25	8	US-10-815-480-1 Sequence 1, Appli
4	24	100.0	25	8	US-10-815-480-2 Sequence 2, Appli
5	24	100.0	25	8	US-10-815-480-7 Sequence 7, Appli
6	24	100.0	25	8	US-10-815-480-8 Sequence 8, Appli
7	24	100.0	48	8	US-10-688-489-73 Sequence 73, Appl
8	24	100.0	51	8	US-10-688-489-84 Sequence 84, Appl
9	24	100.0	70	8	US-10-688-489-72 Sequence 72, Appl
10	24	100.0	71	8	US-10-815-480-71 Sequence 71, Appl
11	24	100.0	10945	7	US-10-361-002-5 Sequence 5, Appli
12	24	100.0	10945	7	US-10-361-004-5 Sequence 5, Appli
13	24	100.0	10975	8	US-10-699-550-1 Sequence 1, Appli
14	24	100.0	11029	8	US-10-699-550-2 Sequence 2, Appli
15	24	100.0	11029	8	US-10-679-520A-66 Sequence 66, Appl
16	24	100.0	11029	9	US-10-706-892-1 Sequence 1, Appli
17	24	100.0	11029	9	US-10-985-805-1 Sequence 1, Appli
18	24	100.0	11029	9	US-10-956-085-1 Sequence 1, Appli
19	23	95.8	23	8	US-10-688-489-76 Sequence 76, Appl
20	23	95.8	50	8	US-10-688-489-85 Sequence 85, Appl
21	22.4	93.3	11029	9	US-10-706-892-2 Sequence 2, Appli
22	22	91.7	22	8	US-10-688-489-77 Sequence 77, Appl
23	22	91.7	49	8	US-10-688-489-86 Sequence 86, Appl

24 21 87.5 21 9 US-10-985-805-53 Sequence 53, Appl
25 21 87.5 23 8 US-10-688-489-149 Sequence 149, App
c 26 19 79.2 19 8 US-10-688-489-116 Sequence 116, App
c 27 19 79.2 87 8 US-10-688-489-101 Sequence 101, App
28 17.8 74.2 434 7 US-10-425-114-6462 Sequence 6462, Ap
c 29 17.8 74.2 592 4 US-09-925-065A-261547 Sequence 261547,
30 17.8 74.2 1831 7 US-10-424-599-28488 Sequence 28488, A
c 31 17.6 73.3 1661 6 US-10-225-066A-1045 Sequence 1045, Ap
c 32 17.6 73.3 1661 6 US-10-302-267-29 Sequence 29, Appl
c 33 17.6 73.3 1661 7 US-10-374-780A-2387 Sequence 2387, Ap
c 34 17.6 73.3 1661 7 US-10-412-699B-411 Sequence 411, App
c 35 17.6 73.3 1661 9 US-10-225-066A-1045 Sequence 1045, Ap
c 36 17.6 73.3 1727 7 US-10-425-114-12992 Sequence 12992, A
c 37 17.2 71.7 2060 7 US-10-424-599-83676 Sequence 83676, A
c 38 16.8 70.0 26 8 US-10-815-480-4 Sequence 4, Appli
c 39 16.8 70.0 487 3 US-09-918-995-5377 Sequence 5377, Ap
c 40 16.8 70.0 704 7 US-10-437-963-21306 Sequence 80309, A
41 16.8 70.0 1416 7 US-10-437-963-21306 Sequence 21906, A
42 16.8 70.0 2802 7 US-10-261-175A-3 Sequence 3, Appli
43 16.8 70.0 33488 6 US-10-085-117-235 Sequence 235, App
44 16.8 70.0 135827 7 US-10-322-281-232 Sequence 232, App
c 45 16.6 69.2 25 7 US-10-719-956-639573 Sequence 639573,

ALIGNMENTS

RESULT 1
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Darby, Paul M.
; APPLICANT: Dennis, Geoffrey G.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GPI40-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-74

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTTCCTGAGGCTTAC 24
|||||
Db 1 TCCGAGACGGTTCCTGAGGCTTAC 24

RESULT 2
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-75

Query Match      100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 1 TCCGAGACGGTCTGAGGGCTTAC 24

RESULT 3
US-10-815-480-1/c
; Sequence 1, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:region of
; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genomes of flaviviruses
US-10-815-480-1

Query Match      100.0%; Score 24; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 24 TCCGAGACGGTCTGAGGGCTTAC 1

RESULT 4
US-10-815-480-2
; Sequence 2, Application US/10815480
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; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:complement to
; OTHER INFORMATION: SEQ ID NO:1
US-10-815-480-2

Query Match      100.0%; Score 24; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 2 TCCGAGACGGTCTGAGGGCTTAC 25

RESULT 5
US-10-815-480-7/c
; Sequence 7, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Koutango virus
; OTHER INFORMATION: Primer 1
US-10-815-480-7

Query Match      100.0%; Score 24; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTCTGAGGGCTTAC 24
Db 24 TCCGAGACGGTCTGAGGGCTTAC 1
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RESULT 6
US-10-815-480-8/c
; Sequence 8, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; TITLE OF INVENTION: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-00023005
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Example Primer
; OTHER INFORMATION: 1
US-10-815-480-8

Query Match 100.0%; Score 24; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGCGCTTAC 24
|||||
Db 24 TCCGAGACGGTCTCTGAGGCGCTTAC 1

RESULT 7
US-10-688-489-73
; Sequence 73, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 48
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-73

Query Match 100.0%; Score 24; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGCGCTTAC 24
|||||
Db 1 TCCGAGACGGTCTCTGAGGCGCTTAC 24

RESULT 8
US-10-688-489-84
; Sequence 84, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (28)..(51)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-84

Query Match 100.0%; Score 24; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGCGCTTAC 24
|||||
Db 28 TCCGAGACGGTCTCTGAGGCGCTTAC 51

RESULT 9
US-10-688-489-72
; Sequence 72, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
US-10-688-489-72

; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 70
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-72

Query Match 100.0%; Score 24; DB 8; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
|||||
DB 1 TCCGAGACGGTCTCGAGGCTTAC 24

RESULT 10
US-10-815-480-71/c
; Sequence 71, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 71
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: region of
; OTHER INFORMATION: conserved sequence in 3' untranslated region of
; OTHER INFORMATION: the genome of flavivirus AF196835
US-10-815-480-71

Query Match 100.0%; Score 24; DB 8; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
68 TCCGAGACGGTCTCGAGGCTTAC 45

RESULT 11
US-10-361-002-5/c
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Pathogen Inactivation Assay
; FILE REFERENCE: CI-0043
; CURRENT APPLICATION NUMBER: US/10/361,002
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patent In version 3.2

; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-002-5

Query Match 100.0%; Score 24; DB 7; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
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DB 10587 TCCGAGACGGTCTCGAGGCTTAC 10564

RESULT 12
US-10-361-004-5/c
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja
; APPLICANT: Marlowe, Kristina
; APPLICANT: Armistead, David
; TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons
; FILE REFERENCE: CI-0042
; CURRENT APPLICATION NUMBER: US/10/361,004
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 10945
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-361-004-5

Query Match 100.0%; Score 24; DB 7; Length 10945;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTAC 24
|||||
DB 10587 TCCGAGACGGTCTCGAGGCTTAC 10564

RESULT 13
US-10-699-550-1/c
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 1
; LENGTH: 10975

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; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-1

Query Match      100.0%; Score 24; DB 8; Length 10975;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 10611 TCCGAGACGGTCTCTGAGGGCTTAC 10588

RESULT 14
US-10-699-550-2/c
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-699-550-2

Query Match      100.0%; Score 24; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
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Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

Query Match      100.0%; Score 24; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

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Job time : 305.582 secs

; PRIOR APPLICATION NUMBER: PR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match      100.0%; Score 24; DB 8; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
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Db 10629 TCCGAGACGGTCTCTGAGGGCTTAC 10606

; PRIOR APPLICATION NUMBER: PR 01/04737
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-679-520A-66

Query Match      100.0%; Score 24; DB 8; Length 10975;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCTGAGGGCTTAC 24
|||||
Db 10611 TCCGAGACGGTCTCTGAGGGCTTAC 10588

RESULT 15
US-10-679-520A-66/c
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE FRANCIS
; APPLICANT: MINKE, JULES WAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.4
; CURRENT APPLICATION NUMBER: US/10/679,520A
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
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Title: US-10-688-489-74

Perfect score: 24

Sequence: 1 tccgagacgggtctgaggccttac 24

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	16.8	70.0	1509	6	US-10-750-185-26120
C 3	16.8	70.0	1692	6	US-10-750-185-60065
C 4	16	66.7	1138	6	US-10-750-185-59175
C 5	16	66.7	2259	7	US-11-000-463-39
C 6	15.6	65.0	4252	6	US-10-750-185-59992
C 7	15.6	65.0	5371	6	US-10-821-234-274
C 8	15.6	65.0	5390	6	US-10-849-438-4
C 9	15.6	65.0	135019	6	US-10-849-438-11
C 10	15.6	65.0	151169	7	US-11-121-086-38
C 11	15.4	64.2	19	8	US-11-101-244-668857
C 12	15.4	64.2	19	9	US-11-083-784-668857
C 13	15.4	64.2	20	6	US-10-849-438-42
C 14	15.2	63.3	429	6	US-10-467-657-273
C 15	15.2	63.3	429	6	US-10-467-657-3719
C 16	15.2	63.3	600	6	US-10-750-185-83
C 17	15.2	63.3	600	6	US-10-750-185-2361
C 18	15.2	63.3	600	6	US-10-750-185-2446
C 19	15.2	63.3	1302	6	US-10-750-185-58252
C 20	15.2	63.3	1414	6	US-10-750-185-44989
C 21	15.2	63.3	1551	6	US-10-750-185-36404
C 22	15.2	63.3	1665	7	US-11-102-240-85
C 23	15.2	63.3	1939	7	US-11-000-463-164

ALIGNMENTS

RESULT 1

US-10-714-781A-66/c
; Sequence 66, Application US/10714781A
; Publication No. US20050255127A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714, 781A
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679,520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676,502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97) ..(10395)
US-10-714-781A-66

Query Match 100.0%; Score 24; DB 6; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGCTTAC 24

Db 10629 TCCGAGACGGTCTCGAGGCTTAC 10606

RESULT 2

US-10-750-185-26120/c
; Sequence 26120, Application US/10750185

Sequence 636, App
Sequence 46042, A
Sequence 47722, A
Sequence 47, Appl
Sequence 49, Appl
Sequence 51, Appl
Sequence 662, App
Sequence 24, Appl
Sequence 35820, A
Sequence 42703, A
Sequence 1, Appl
Sequence 49, Appl
Sequence 32, Appl
Sequence 48, Appl
Sequence 52, Appl
Sequence 3455, Ap
Sequence 4805, Ap
Sequence 40960, A
Sequence 66, Appl
Sequence 61751, A
Sequence 50493, A

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; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 26120
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Bovine 19866880728422
US-10-750-185-26120
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Query Match 70.0%; Score 16.8; DB 6; Length 1509;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAGACGGTCTCGAGGGCT 21
Db 359 CCGAGCGGTTCTCGGGCT 340
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RESULT 3
US-10-750-185-60065
; Sequence 60065, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 60065
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: Bovine 19866880728422
US-10-750-185-60065
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Query Match 70.0%; Score 16.8; DB 6; Length 1692;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGC 20
Db 677 TCCGAGCGCTTCTGAGGC 696
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RESULT 4
US-10-750-185-59175
; Sequence 59175, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
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; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59175
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Bovine 19866880752265
US-10-750-185-59175
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Query Match 66.7%; Score 16; DB 6; Length 1138;
Best Local Similarity 79.2%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTCGAGGGTTAC 24
Db 1039 TCAGAGACGATTCTGAGCACTTC 1062
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RESULT 5
US-11-000-463-39/c
; Sequence 39, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radolje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2259
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (182)..(1078)
US-11-000-463-39
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QY 2 CCGAGACGGTCTGAGGGCTTA 23

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: 060002009438R1
: GENERAL INFORMATION:
: APPLICANT: FOULSEN, TIM S.
: APPLICANT: NIELSEN, KIRSTEN V.
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEOTIC ACID ANALOG PROBES
: FILE REFERENCE: 09138.6000-00000
: CURRENT APPLICATION NUMBER: US/11/121,086
: CURRENT FILING DATE: 2005-05-04

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RESULT 12
US-11-083-784-668857
; Sequence 668857, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacon, Inc.
; APPLICANT: Khavrova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Searings, Stephen
; TITLE OF INVENTION: Functional and Hypo
; FILE REFERENCE: J3499US
; CURRENT APPLICATION NUMBER: US/11/083, 7
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714, 333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502, 050

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RESULT 14
US-10-467-657-273
; Sequence 273, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 273
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-273

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Query Match 63.3%; Score 15.2; DB 6; Length 429;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGAGACGGTCTGAGGGC 20
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 Db 7 TCCGAACCGATTGAGGGC 26

RESULT 15
 US-10-467-657-3719
 ; Sequence 3719, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; PRIOR FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 3719
 ; LENGTH: 429
 ; TYPE: DNA
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-3719

Query Match 63.3%; Score 15.2; DB 6; Length 429;
 Best Local Similarity 85.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 7 TCCGAACCGATTGAGGGC 26

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Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score: 24
Sequence: 1 tcgcagacggtcttgagggttac 24

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Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

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10: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	10	41.7	23	7 US-11-186-497-19	Sequence 19, Appl
C 2	9	37.5	22	6 US-10-750-185-10657	Sequence 10657, A
C 3	9	37.5	22	7 US-11-069-908-2047	Sequence 2047, Ap
C 4	9	37.5	22	7 US-11-069-908-4146	Sequence 4146, Ap
C 5	9	37.5	22	7 US-11-069-908-4852	Sequence 4852, Ap
C 6	9	37.5	22	7 US-11-069-908-5595	Sequence 5595, Ap
C 7	9	37.5	23	7 US-11-072-031-2	Sequence 2, Appli
C 8	8	33.3	22	6 US-10-500-831-32	Sequence 32, Appl
C 9	8	33.3	22	6 US-10-500-831-185	Sequence 185, App
C 10	8	33.3	22	6 US-10-477-950-12	Sequence 12, Appl
C 11	8	33.3	22	6 US-10-524-643-91	Sequence 91, Appl
C 12	8	33.3	22	6 US-10-750-185-10054	Sequence 10054, A
C 13	8	33.3	22	6 US-10-750-185-11416	Sequence 11416, A
C 14	8	33.3	22	6 US-10-750-185-11416	Sequence 11416, A
C 15	8	33.3	22	6 US-10-750-185-12782	Sequence 12782, A
C 16	8	33.3	22	6 US-10-750-185-12782	Sequence 13800, A
C 17	8	33.3	22	7 US-11-102-228-6	Sequence 6, Appli
C 18	8	33.3	22	7 US-11-069-908-374	Sequence 374, App
C 19	8	33.3	22	7 US-11-069-908-1363	Sequence 1363, Ap
C 20	8	33.3	22	7 US-11-069-908-1475	Sequence 1475, Ap
C 21	8	33.3	22	7 US-11-069-908-1780	Sequence 1780, Ap
C 22	8	33.3	22	7 US-11-069-908-3729	Sequence 3729, Ap
C 23	8	33.3	22	7 US-11-069-908-3841	Sequence 3841, Ap

C 24	8	33.3	22	7 US-11-069-908-4413	Sequence 4413, Ap
C 25	8	33.3	22	7 US-11-069-908-5076	Sequence 5076, Ap
C 26	8	33.3	22	7 US-11-069-908-6891	Sequence 6891, Ap
C 27	8	33.3	22	7 US-11-069-908-6954	Sequence 6954, Ap
C 28	8	33.3	22	7 US-11-083-538-12	Sequence 12, Appl
C 29	8	33.3	23	6 US-10-750-185-12555	Sequence 12555, A
C 30	8	33.3	23	6 US-10-750-185-13190	Sequence 13190, A
C 31	8	33.3	23	6 US-10-750-185-14244	Sequence 14244, A
C 32	8	33.3	23	6 US-10-750-185-14506	Sequence 14506, A
C 33	8	33.3	23	6 US-10-750-185-14794	Sequence 14794, A
C 34	8	33.3	23	6 US-10-750-185-16082	Sequence 16082, A
C 35	8	33.3	23	7 US-11-043-959-30	Sequence 30, Appl
C 36	8	33.3	23	7 US-11-052-544-23	Sequence 23, Appl
C 37	8	33.3	23	7 US-11-049-830-1	Sequence 1, Appli
C 38	8	33.3	23	7 US-11-072-031-47	Sequence 47, Appl
C 39	8	33.3	23	7 US-11-072-031-185	Sequence 185, App
C 40	8	33.3	23	7 US-11-090-739-106	Sequence 106, App
C 41	8	33.3	23	7 US-11-069-908-2020	Sequence 2020, Ap
C 42	8	33.3	23	7 US-11-069-908-4386	Sequence 4386, Ap
C 43	8	33.3	23	9 US-11-096-706-218	Sequence 218, App
C 44	8	33.3	24	6 US-10-500-831-9	Sequence 9, Appli
C 45	8	33.3	24	6 US-10-500-831-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-11-186-497-19/c
; Sequence 19, Application US/11186497
; Publication No. US20050255597A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/186,497
; FILING DATE: 21-JULY-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-11-186-497-19

Query Match 41.7%; Score 10; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGCT 21
|||||
DB 21 TCTGAGGGCT 12

RESULT 2

US-10-750-185-10657/c
; Sequence 10657, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10657
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer

US-10-750-185-10657

Query Match 37.5%; Score 9; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAGG 18
|||||
DB 10 GTTCTGAGG 2

RESULT 3

US-11-069-908-2047/c
; Sequence 2047, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MURRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; FILE REFERENCE: 029011-0402
; CURRENT APPLICATION NUMBER: US/11/069,908
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/547,823
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7098
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2047
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

US-11-069-908-2047

Query Match 37.5%; Score 9; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCTGAGGGC 20
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DB 22 TCTGAGGGC 14

RESULT 4

US-11-069-908-4146/c
; Sequence 4146, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MURRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; FILE REFERENCE: 029011-0402
; CURRENT APPLICATION NUMBER: US/11/069,908
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/547,823
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7098
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4146
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

US-11-069-908-4146

Query Match 37.5%; Score 9; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGTTCTGA 16
|||||
DB 22 CGGTTCTGA 14

RESULT 5

US-11-069-908-4852
; Sequence 4852, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MURRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; FILE REFERENCE: 029011-0402
; CURRENT APPLICATION NUMBER: US/11/069,908
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/547,823
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7098
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4852
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

US-11-069-908-4852

Query Match 37.5%; Score 9; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CTGAGGGCT 21


```
Db      3 CTGAGGCGT 11
|||||
RESULT 6
US-11-069-908-5595
; Sequence 5595, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
; APPLICANT: OLIPHANT, ARNOLD
; APPLICANT: MURRAY, SARAH
; TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
; FILE REFERENCE: 029011-0402
; CURRENT APPLICATION NUMBER: US/11/069,908
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/547,823
; PRIOR FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7098
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5595
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-5595
Query Match      37.5%; Score 9; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TTCTGAGGG 19
Db      12 TTCTGAGGG 20
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RESULT 7
US-11-072-031-2
; Sequence 2, Application US/11072031
; Publication No. US20050261222A1
; GENERAL INFORMATION:
; APPLICANT: Beiersdorf AG, Hamburg
; APPLICANT: Wolber, Rainer
; APPLICANT: Kolbe, Lüdger
; APPLICANT: Mundt, Claudia
; APPLICANT: Gallinat, Stefan
; APPLICANT: Breitenbach, Ute
; TITLE OF INVENTION: Oligonucleotides for the Treatment of Irritative or Inflammatory
; FILE REFERENCE: 104035/269168
; CURRENT APPLICATION NUMBER: US/11/072,031
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: DE 102004010547.2
; PRIOR FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-031-2
Query Match      37.5%; Score 9; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGACGGTT 12
Db      15 GAGACGGTT 23
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RESULT 8
US-11-072-031-2
; Sequence 3, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-32
Query Match      33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGTTCTG 15
Db      14 CGGTTCTG 7
|||||
RESULT 9
US-10-500-831-185/c
; Sequence 185, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 185
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-185
Query Match      33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGTTCTG 15
Db      14 CGGTTCTG 7
|||||
RESULT 10
US-10-477-950-12
; Sequence 12, Application US/10477950
; Publication No. US20050260207A1
; GENERAL INFORMATION:
; APPLICANT: Krka tovarna zdravil, d.d., Novo mesto
; TITLE OF INVENTION: Monoclonal antibody neutralising Cathepsin B activity
; FILE REFERENCE: 28880
; CURRENT APPLICATION NUMBER: US/10/477,950
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: SI/P200100132
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; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Mouse
US-10-477-950-12

Query Match 33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACGGT 11
|||||
DB 15 GAGACGGT 22

RESULT 11
US-10-524-643-91
; Sequence 91, Application US/10524643
; Publication No. US20050261215A1
; GENERAL INFORMATION:
; APPLICANT: GARREN, Hideki
; APPLICANT: HO, Peggy P.
; APPLICANT: STEINMAN, Lawrence
; TITLE OF INVENTION: METHODS AND IMMUNE MODULATORY NUCLEIC ACID COMPOSITIONS FOR
; PREVENTING AND TREATING DISEASE
; FILE REFERENCE: 022259-001010US
; CURRENT APPLICATION NUMBER: US/10/524,643
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US2003/037157
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunomodulatory oligonucleotide
US-10-524-643-91

Query Match 33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TGAGGGCT 21
|||||
DB 7 TGAGGGCT 14

RESULT 12
US-10-750-185-10054/c
; Sequence 10054, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10054

; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-10054

Query Match 33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGGCGTTA 23
|||||
DB 18 AGGCGTTA 11

RESULT 13
US-10-750-185-11416
; Sequence 11416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11416
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-11416

Query Match 33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCTGAG 17
|||||
DB 1 GTTCTGAG 8

RESULT 14
US-10-750-185-11416/c
; Sequence 11416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 11416
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-11416

Query Match      33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCCGAGAC 8
Db      15 TCCGAGAC 8
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RESULT 15
US-10-750-185-12782/c
; Sequence 12782, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12782
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-12782
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Query Match      33.3%; Score 8; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TTCTGAGG 18
Db      14 TTCTGAGG 7
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Search completed: December 12, 2005, 04:33:49
Job time : 372 secs

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